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2 0 NOV 2006

Docket No. 12810-00067-US  
(PATENT)

Legal Staff  
International Division

**IN THE UNITED STATES PATENT AND TRADEMARK OFFICE**

In re Patent Application of:  
Karl-Heinz Kogel et al.

Application No.: 10/522,106

Confirmation No.: 9243

Filed: January 24, 2005

Art Unit: N/A

For: METHOD FOR OBTAINING THE  
PATHOGENIC RESISTANCE IN PLANTS

Examiner: Not Yet Assigned

**REQUEST FOR RECONSIDERATION**

MS PCT Legal Affairs  
Commissioner for Patents  
P.O. Box 1450  
Alexandria, VA 22313-1450

Dear Sir:

The Applicants respectfully request reconsideration of the Decision on Petition mailed October 2, 2006. Applicants respectfully request reconsideration of the Request for Withdrawal of Holding of Abandonment, or in the alternative that the Petition under 37 CFR § 1.137 (b) be granted, and the application be forwarded to the Examiner for Examination.

**I. Request For Reconsideration of the Request for Withdrawal of Holding of Abandonment**

In the Decision On Petition mailed October 2, 2006, the PCT Legal Examiner asserted that because the "Assignment of Application" allegedly did not specifically identify the application being assigned, that the submission of Power of Attorney and change of correspondence address submission of June 3, 2005, "did not properly establish the right of the assignee to take action in this case, and so the submission was not effective in changing the pre-existing correspondence address of record." Applicants respectfully disagree and strongly urge reconsideration of the Request for the following reasons.

1. The "Assignment of Application" was submitted with the initial filing of the application on January 24, 2005, as evidenced by the date on the Recordation Form Cover Sheet (attached as Exhibit 1 with the "Assignment of Application"; previously submitted in the Request for Withdrawal of Holding of Abandonment filed on April 28, 2006 as part of Exhibit A). The date on the cover sheet is January 24, 2005, which is the same as the date of filing of the application. The U.S. application number could only be given out after the initial filing of the application. Therefore, on the initial filing date of the application which included the "Assignment of Application" with the proper cover sheet, it would have been impossible for the U.S. application number to be indicated.

2. The inventors signed the "Assignment of Application" on July 30, 2003, shortly after the international filing date of July 14, 2003, assigning their entire rights to BASF Plant Science GmbH. Therefore, at the time of filing the U.S. national stage application on January 24, 2005, the "Assignment of Application" was already executed and could not have specifically identified the application by its U.S. application number.

3. Furthermore, toward the top right hand corner of each page of the "Assignment of Application" document, the number "0000053765" is printed (see Exhibit 1). This number represents the assignee's internal docket number. This same number also appears as a header on the specification as filed. This same number also appears on the top right hand corner of each page of the "Declaration, Power of Attorney and Petition" (attached as Exhibit 2). This Declaration was signed by the inventors on the same day as the "Assignment of Application" on July 30, 2003 and was also submitted to the U. S. Patent and Trademark Office with the initial filing of the application on January 24, 2005. Therefore, the "Assignment of Application" does specifically identify the application which is being assigned, contrary to the Examiner's assertion.

4. Since the Power of Attorney and change of correspondence address submission of June 3, 2005, Applicants received the Notice of Recordation of Assignment Document on November 8, 2005, indicating that the "Assignment of Application" was recorded in the U.S. Patent and Trademark Office on January 24, 2005 (attached as Exhibit 3). Such recordation can be found at Reel/Frame No. 016749/0176. The date of recordation corresponds to the date on the

recordation cover sheet and the date of the initial U.S. filing. The assignee of record is BASF Plant Science GmbH as of January 24, 2005, the date of filing the initial application. Therefore, when the Power of Attorney and change of correspondence address was submitted to the U.S. Patent and Trademark Office, BASF Plant Science GmbH was already the assignee of record with the authority and power to revoke previous powers of attorney and appoint new attorneys pursuant to 37 CFR § 3.71. Furthermore, when the Power of Attorney and change of correspondence address was submitted to the U.S. Patent and Trademark Office, the Transmittal of Power of Attorney indicated that the cover sheet and "Assignment of Application" document were enclosed because the Notice of Recordation had not yet been received and that these had been submitted with the initial filing of the application (as also indicated on the initial Request for Withdrawal of Holding of Abandonment). Therefore, the submission of the Power of Attorney and change of correspondence address was not to establish the rights of the assignee, since these were already established with the initial filing of the application, but to appoint new attorneys and change the correspondence address. Additionally, as required, a Statement under 37 CFR § 3.73(b) and a duly completed and executed "Power of Attorney to Prosecute Applications Before the USPTO" form were submitted pursuant to 37 CFR § 3.71 with the Transmittal of Power of Attorney.

5. Because the "Assignment of Application" was submitted with the initial filing of the application and identified the application by number, which number is found on the executed Declaration (Exhibit 2) and in the application as filed and because the "Assignment of Application" was duly recorded as of the application initial filing date of January 24, 2005 (as evidenced on the Notice of Recordation, Exhibit 3), Applicants submit that the Power of Attorney and change of correspondence address of June 3, 2005 appointing Connolly Bove Lodge & Hutz LLP was properly submitted by the assignee of record, BASF Plant Science GmbH.

6. A Notice of Missing Parts was mailed July 1, 2005 to Morrison & Foerster. BASF Plant Science GmbH appointed Connolly Bove Lodge & Hutz LLP with the Power of Attorney and change of correspondence address submission of June 3, 2005. Therefore, the Notice of Missing Parts was mailed to the incorrect address of record, which ultimately caused the application to go abandoned.

Applicants respectfully submit that the "Assignment of Application" submitted with the initial filing of the application on January 24, 2005 was effective in establishing the right of the assignee to take action in this case, for the reasons explained above.

Applicants respectfully request reconsideration of the Request for Withdrawal of Holding of Abandonment, because Applicants submitted a proper Power of Attorney with change of correspondence address, as explained above, prior to the mailing of the Notice of Missing Parts. Accordingly, Applicants also request reimbursement of the petition fee under § 1.17(m).

## **II. In the Alternative, Reconsideration of the Petition under 37 C.F.R. § 1.137 (b)**

Further to the Decision On Petition mailed October 2, 2006, Applicants submit herewith a proper reply to the Notification to Comply with Requirements for Patent Applications Containing Nucleotide and/or Amino Acid Sequence Disclosures which the Examiner kindly provided with their Decision On Petition. The Reply consists of a copy of the Notification to Comply, a Response to the Notification to Comply and Amendment, a replacement paper copy of the Sequence Listing which conforms to 37 CFR §§ 1.821-1.825, a diskette containing the Sequence Listing in computer readable form, and a Statement to Support Filing and Submission in Accordance with 37 CFR §§ 1.821-1.825.

Although Applicants strongly urge reconsideration of the Request for Withdrawal of Holding of Abandonment, in the alternative, Applicants request that the Application be revived. The Petition fee has been paid. Applicants state that the entire delay in filing the required reply from the due date for the reply until the filing of a grantable petition pursuant 37 CFR § 1.137(b)(3) was unintentional. Applicants submit that with the attached reply all requirements under 37 CFR § 1.137(b) have been met.

Furthermore, Applicants respectfully request that a Notice of Acceptance of Power of Attorney be issued and the correspondence address be appropriately changed. If the Examiner finds that the Power of Attorney and change of correspondence address is not effective in

making these changes, then Applicants respectfully request assistance in what further would be required.

This response is filed within the two-month period for response from the mailing of the Decision on Petition, to and including December 4, 2006, pursuant to 37 CFR § 1.7(a). No fee is believed due. However, if a fee is due, the Commissioner is hereby authorized to charge or credit our Deposit Account No. 03-2775, under Order No. 12810-00067-US from which the undersigned is authorized to draw.

A prompt and favorable action is earnestly solicited.

Respectfully submitted,

By 

Roberte M. D. Makowski

Registration No.: 55,421

CONNOLLY BOVE LODGE & HUTZ LLP

Correspondence Customer Number: 23416

1007 North Orange Street, P.O. Box 2207

Wilmington, Delaware 19899

(302) 888-6410 (Tel), (302) 658-5614 (Fax)

Attorney for Applicants

#8

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20 NOV 2006

PTO/SB/92 (09-04)

Approved for use through 07/31/2006. OMB 0651-0031

U.S. Patent and Trademark Office; U.S. DEPARTMENT OF COMMERCE

Under the Paperwork Reduction Act of 1995, no persons are required to respond to a collection of information unless it displays a valid OMB control number.

Legal Staff  
International Division  
Application No.: 10/522,106

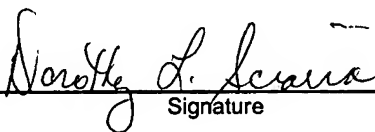
Attorney Docket No.: 12810-00067-US

## Certificate of Mailing under 37 CFR 1.8

I hereby certify that this correspondence is being deposited with the United States Postal Service with sufficient postage as first class mail in an envelope addressed to:

MS PCT  
**ATTENTION : PCT Legal Office**  
Commissioner for Patents  
P.O. Box 1450  
Alexandria, VA 22313-1450

on November 15, 2006  
Date

  
Signature

Dorothy L. Sciarra

Typed or printed name of person signing Certificate

Registration Number, if applicable

(302) 658-9141  
Telephone Number

Note: Each paper must have its own certificate of mailing, or this certificate must identify each submitted paper.

Request for Reconsideration (5 pages)  
Exhibit 1 – Recordation Form Cover Sheet and Assignment of Application (3 pages)  
Exhibit 2 – Declaration, Power of Attorney and Petition (3 pages)  
Exhibit 3 – Notice of Recordation and Assignment Document (3 pages)  
Response to Notification to Comply with Requirements for Patent Applications  
Containing Nucleotide and/or Amino Acid Sequence Disclosures and Amendment (3  
pages)  
Copy of Notification to Comply with Requirements for Patent Applications Containing  
Nucleotide and/or Amino Acid Sequence Disclosures (9 pages)  
Sequence Listing (CRF copy – 1 Disk and Paper copy (54 pages))  
Statement to Support Filing and Submission in Accordance with 37 CFR §§1.821  
through 1.825 (2 pages)  
Certificate of Mailing (1 page)  
Postcard



## UNITED STATES PATENT AND TRADEMARK OFFICE

UNITED STATES DEPARTMENT OF COMMERCE  
 United States Patent and Trademark Office  
 Address: COMMISSIONER FOR PATENTS  
 P.O. Box 1450  
 Alexandria, Virginia 22313-1450  
 www.uspto.gov

U.S. APPLICATION NUMBER NO.	FIRST NAMED APPLICANT	ATTY. DOCKET NO.
10/522,106	Karl-Heinz Kogel	532622010500

INTERNATIONAL APPLICATION NO.	
PCT/EP03/07589	
I.A. FILING DATE	PRIORITY DATE
07/14/2003	

Morrison & Foerster  
 1650 Tysons Boulevard, Suite 300  
 McLean, VA 22102

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20 NOV 2006

Legal Staff  
 International Division

CONFIRMATION NO. 9243  
 371 FORMALITIES LETTER



\*OC000000016430884\*

Date Mailed: 07/01/2005

### NOTIFICATION TO COMPLY WITH REQUIREMENTS FOR PATENT APPLICATIONS CONTAINING NUCLEOTIDE AND/OR AMINO ACID SEQUENCE DISCLOSURES

Applicant is given **TWO MONTHS FROM THE DATE OF THIS NOTICE** within which to file the items indicated below to avoid abandonment. Extensions of time may be obtained under the provisions of 37 CFR 1.136(a).

- A copy of the "Sequence Listing" in computer readable form has been submitted. However, the content of the computer readable form does not comply with the requirements of 37 CFR 1.822 and/or 1.823, as indicated on the attached copy of the marked -up "Raw Sequence Listing." Applicant must provide a substitute computer readable form (CRF) copy of the "Sequence Listing" and a statement that the content of the sequence listing information recorded in computer readable form is identical to the written (on paper or compact disc) sequence listing and, where applicable, includes no new matter, as required by 37 CFR 1.821(e), 1.821(f), 1.821(g), 1.825(b), or 1.825(d).

Applicant is cautioned that correction of the above items may cause the specification and drawings page count to exceed 100 pages. If the specification and drawings exceed 100 pages, applicant will need to submit the required application size fee.

For questions regarding compliance to 37 CFR 1.821-1.825 requirements, please contact:

- For Rules Interpretation, call (571) 272-0951
- For Patent Software Program Help, call Patent EBC at 1-866-217-9197 or directly at 703-305-3028 / 703-308-6845 between the hours of 6 a.m. and 12 midnight, Monday through Friday, EST.
- Send e-mail correspondence for Patent Software Program Help @ [ebc@uspto.gov](mailto:ebc@uspto.gov)

Applicant is reminded that any communications to the United States Patent and Trademark Office must be mailed to the address given in the heading and include the U.S. application no. shown above (37 CFR 1.5)

*A copy of this notice **MUST** be returned with the response.*

LAMONT M HUNTER

Telephone: (703) 308-9140 EXT 201

## PART 2 - OFFICE COPY

U.S. APPLICATION NUMBER NO.	INTERNATIONAL APPLICATION NO.	ATTY. DOCKET NO.
10/522,106	PCT/EP03/07589	532622010500

FORM PCT/DO/EO/922 (371 Formalities Notice)



## STIC Biotechnology Systems Branch

### RAW SEQUENCE LISTING ERROR REPORT

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: 10/522,106

Source: PCT

Date Processed by STIC: 2-2-05

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.

PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:

- 1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,
- 2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY

FOR CRF SUBMISSION AND PATENTIN SOFTWARE QUESTIONS, PLEASE CONTACT MARK SPENCER, TELEPHONE: 571-272-2510; FAX: 571-273-0221

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE CHECKER VERSION 4.2.2 PROGRAM, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW FOR ADDRESS:

<http://www.uspto.gov/web/offices/pac/checker/chkrnote.htm>

Applicants submitting genetic sequence information electronically on diskette or CD-Rom should be aware that there is a possibility that the disk/CD-Rom may have been affected by treatment given to all incoming mail.

Please consider using alternate methods of submission for the disk/CD-Rom or replacement disk/CD-Rom.

Any reply including a sequence listing in electronic form should NOT be sent to the 20231 zip code address for the United States Patent and Trademark Office, and instead should be sent via the following to the indicated addresses:

1. EFS-Bio (<<http://www.uspto.gov/ebs/efs/downloads/documents.htm>> , EFS Submission User Manual - ePAVE)
2. U.S. Postal Service: Commissioner for Patents, P.O. Box 1450, Alexandria, VA 22313-1450
3. Hand Carry, Federal Express, United Parcel Service, or other delivery service (EFFECTIVE 01/14/05):  
U.S. Patent and Trademark Office, Mail Stop Sequence, Customer Window, Randolph Building, 401 Dulany Street, Alexandria, VA 22314

Revised 01/24/05



PCT

## RAW SEQUENCE LISTING

DATE: 02/02/2005

PATENT APPLICATION: US/10/522,106

TIME: 15:31:41

Input Set : A:\Sequence Listing.txt

Output Set: N:\CRF4\02022005\J522106.raw

2 <110> APPLICANT: Kogel, Karl-Heinz  
 3 Huckelhoven, Ralph  
 4 Trujillo, Marco  
 6 <120> TITLE OF INVENTION: Method for Obtaining a Pathogen Resistance in Plants  
 8 <130> FILE REFERENCE: 532622010500  
 C--> 10 <140> CURRENT APPLICATION NUMBER: US/10/522,106  
 11 <141> CURRENT FILING DATE: 2005-01-24  
 13 <160> NUMBER OF SEQ ID NOS: 24  
 14 <170> SOFTWARE: PatentIn Ver. 2.1

## ERRORED SEQUENCES

45 <210> SEQ ID NO: 2  
 46 <211> LENGTH: 112  
 47 <212> TYPE: PRT  
 48 <213> ORGANISM: Hordeum vulgare  
 W--> 49 <400> SEQUENCE: 2  
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 51 1 5 10 15  
 52 Ile Glu Met His Asn Tyr Leu Thr Ser Val Tyr Glu Glu Gly Asp Ala  
 53 20 25 30  
 54 Arg Ser Ala Leu Ile Thr Met Leu Gln Ala Leu Asn His Ala Lys Asn  
 55 35 40 45  
 E--> 56 Gly Val Asp Val Val Ser Xaa Thr Arg Val Arg Thr His Phe Ala Arg  
 57 50 55 60  
 58 Pro Asn Phe Lys Arg Val Leu Ser Lys Val Ala Ala Lys His Pro Tyr  
 59 65 70 75 80  
 60 Ala Lys Ile Gly Val Phe Tyr Cys Gly Ala Pro Val Leu Ala Gln Glu  
 61 85 90 95  
 62 Leu Ser Asn Leu Cys His Glu Phe Asn Gly Lys Cys Thr Thr Lys Phe  
 63 100 105 110  
 2181 <210> SEQ ID NO: 16  
 2182 <211> LENGTH: 939  
 2183 <212> TYPE: PRT  
 2184 <213> ORGANISM: Nicotiana tabacum  
 W--> 2185 <400> SEQUENCE: 16  
 2186 Met Gln Asn Ser Glu Asn His His Pro His His Gln His His His Ser  
 2187 1 5 10 15  
 2188 Asp Thr Glu Ile Ile Gly Asn Asp Arg Ala Ser Tyr Ser Gly Pro Leu  
 2189 20 25 30  
 2190 Ser Gly Pro Leu Asn Lys Arg Gly Gly Lys Lys Ser Ala Arg Phe Asn  
 2191 35 40 45

*pls explain*  
*"Xaa" location. Does Not Comply*  
*Corrected Diskette Needed*  
*(P5.1, 3)*  
*See error explanation*  
*on page 5.*

## RAW SEQUENCE LISTING

DATE: 02/02/2005

PATENT APPLICATION: US/10/522,106

TIME: 15:31:42

Input Set : A:\Sequence Listing.txt

Output Set: N:\CRF4\02022005\J522106.raw

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2192 Ile Pro Glu Ser Thr Asp Ile Gly Thr Ser Val Gly Thr Gly Gly Lys
2193      50      55      60
2194 Ser Asn Asp Asp Ala Tyr Val Glu Ile Thr Leu Asp Val Arg Glu Asp
2195 65      70      75      80
2196 Ser Val Ala Val His Ser Val Lys Thr Ala Gly Gly Asp Asp Val Glu
2197      85      90      95
2198 Asp Pro Glu Leu Ala Leu Leu Ala Lys Gly Leu Glu Lys Lys Ser Thr
2199      100     105     110
2200 Leu Gly Ser Ser Leu Val Arg Asn Ala Ser Ser Arg Ile Arg Gln Val
2201      115     120     125
2202 Ser Gln Glu Leu Arg Arg Leu Ala Ser Leu Asn Lys Arg Pro Ile Pro
2203      130     135     140
2204 Thr Gly Arg Phe Asp Arg Asn Lys Ser Ala Ala His Ala Leu Lys
2205 145     150     155     160
2206 Gly Leu Lys Phe Ile Ser Lys Thr Asp Gly Gly Ala Gly Trp Ala Ala
2207      165     170     175
2208 Val Glu Lys Arg Phe Asp Glu Ile Thr Ala Ser Thr Thr Gly Leu Leu
2209      180     185     190
2210 Pro Arg Ala Lys Phe Gly Glu Cys Ile Gly Met Asn Lys Glu Ser Lys
2211      195     200     205
2212 Glu Phe Ala Val Glu Leu Tyr Asp Ala Leu Ala Arg Arg Arg Asn Ile
2213      210     215     220
2214 Thr Thr Asp Ser Ile Asn Lys Ala Gln Leu Lys Glu Phe Trp Asp Gln
2215 225     230     235     240
2216 Val Ala Asp Gln Ser Phe Asp Ser Arg Leu Gln Thr Phe Phe Asp Met
2217      245     250     255
2218 Val Asp Lys Asp Ala Asp Gly Arg Ile Thr Glu Glu Glu Val Arg Glu
2219      260     265     270
2220 Ile Ile Gly Leu Ser Ala Ser Ala Asn Arg Leu Ser Thr Ile Gln Lys
2221      275     280     285
2222 Gln Ala Asp Glu Tyr Ala Ala Met Ile Met Glu Glu Leu Asp Pro Asn
2223      290     295     300
2224 Asn Leu Gly Tyr Ile Met Ile Glu Asn Leu Glu Met Leu Leu Leu Gln
2225 305     310     315     320
2226 Ala Pro Asn Gln Ser Val Gln Arg Gly Gly Glu Ser Arg Asn Leu Ser
2227      325     330     335
2228 Gln Met Leu Ser Gln Lys Leu Lys His Thr Gln Glu Arg Asn Pro Ile
2229      340     345     350
2230 Val Arg Trp Tyr Lys Ser Phe Met Tyr Phe Leu Leu Asp Asn Trp Gln
2231      355     360     365
2232 Arg Val Trp Val Leu Leu Leu Trp Ile Gly Ile Met Ala Gly Leu Phe
2233      370     375     380
2234 Thr Trp Lys Tyr Ile Gln Tyr Lys Glu Lys Ala Ala Tyr Lys Val Met
2235 385     390     395     400
2236 Gly Pro Cys Val Cys Phe Ala Lys Gly Ala Ala Glu Thr Leu Lys Leu
2237      405     410     415
2238 Asn Met Ala Ile Ile Leu Phe Pro Val Cys Arg Asn Thr Ile Thr Trp
2239      420     425     430
2240 Leu Arg Asn Lys Thr Arg Leu Gly Ala Ala Val Pro Phe Asp Asp Asn

```

## RAW SEQUENCE LISTING

DATE: 02/02/2005

PATENT APPLICATION: US/10/522,106

TIME: 15:31:42

Input Set : A:\Sequence Listing.txt

Output Set: N:\CRF4\02022005\J522106.raw

2241                    435                    440                    445  
 2242 Leu Asn Phe His Lys Val Ile Ala Val Ala Ile Ala Leu Gly Val Gly  
 2243                    450                    455                    460  
 2244 Ile His Gly Leu Ser His Leu Thr Cys Asp Phe Pro Arg Leu Leu Asn  
 2245 465                    470                    475                    480  
 2246 Ala Ser Glu Glu Glu Tyr Glu Pro Met Lys Tyr Tyr Phe Gly Asp Gln  
 2247                    485                    490                    495  
 2248 Pro Glu Ser Tyr Trp Trp Phe Ile Lys Gly Val Glu Gly Val Thr Gly  
 2249                    500                    505                    510  
 2250 Ile Ile Met Val Val Leu Met Ala Ile Ala Phe Thr Leu Ala Thr Pro  
 2251                    515                    520                    525  
 2252 Trp Phe Arg Arg Asn Arg Val Ser Leu Pro Lys Pro Phe His Lys Leu  
 2253                    530                    535                    540  
 E--> 2254 Thr Gly Xaa Asn Ala Phe Trp Tyr Ser His His Leu Phe Val Ile Val  
 2255 545                    550                    555                    560  
 2256 Tyr Thr Leu Phe Ile Val His Gly Glu Lys Leu Tyr Ile Thr Lys Asp  
 2257                    565                    570                    575  
 2258 Trp Tyr Lys Arg Thr Asp Met Asp Val Leu Leu Thr Ile Pro Ile Ile  
 2259                    580                    585                    590  
 2260 Leu Tyr Ala Ser Glu Arg Leu Ile Arg Ala Phe Arg Ser Ser Ile Lys  
 2261                    595                    600                    605  
 2262 Ala Val Lys Ile Leu Lys Val Ala Val Tyr Pro Gly Asn Val Leu Ala  
 2263                    610                    615                    620  
 2264 Leu His Met Ser Lys Pro Gln Gly Tyr Lys Tyr Lys Ser Gly Gln Tyr  
 2265 625                    630                    635                    640  
 2266 Met Phe Val Asn Cys Ala Ala Val Ser Pro Phe Glu Trp His Pro Phe  
 2267                    645                    650                    655  
 2268 Ser Ile Thr Ser Ala Pro Gly Asp Asp Tyr Leu Ser Val His Ile Arg  
 2269                    660                    665                    670  
 2270 Thr Leu Gly Asp Trp Thr Arg Gln Leu Lys Thr Val Phe Ser Glu Val  
 2271                    675                    680                    685  
 2272 Cys Gln Pro Pro Pro Asn Gly Lys Ser Gly Leu Leu Arg Ala Asp Tyr  
 2273                    690                    695                    700  
 2274 Leu Gln Gly Glu Asn Asn Pro Asn Phe Pro Arg Val Leu Ile Asp Gly  
 2275 705                    710                    715                    720  
 2276 Pro Tyr Gly Ala Pro Ala Gln Asp Tyr Lys Lys Tyr Glu Val Val Leu  
 2277                    725                    730                    735  
 2278 Leu Val Gly Leu Gly Ile Gly Ala Thr Pro Met Ile Ser Ile Val Lys  
 2279                    740                    745                    750  
 2280 Asp Ile Val Asn Asn Met Lys Ala Met Asp Glu Glu Glu Asn Ser Leu  
 2281                    755                    760                    765  
 2282 Glu Asp Gly His Asn Asn Asn Met Ala Pro Asn Ser Ser Pro Asn Ile  
 2283                    770                    775                    780  
 2284 Ala Lys Asn Lys Gly Asn Lys Ser Gly Ser Ala Ser Gly Gly Asn Asn  
 2285 785                    790                    795                    800  
 2286 Phe Asn Thr Arg Arg Ala Tyr Phe Tyr Trp Val Thr Arg Glu Gln Gly  
 2287                    805                    810                    815  
 2288 Ser Phe Asp Trp Phe Lys Gly Ile Met Asn Glu Ala Ala Glu Met Asp  
 2289                    820                    825                    830

←  
 pls  
 explain  
 Xaa location.

pls see  
 error  
 explanation  
 on page 5.

The type of errors shown exist throughout  
 the Sequence Listing. Please check subsequent  
 sequences for similar errors.

## RAW SEQUENCE LISTING

DATE: 02/02/2005

PATENT APPLICATION: US/10/522,106

TIME: 15:31:42

Input Set : A:\Sequence Listing.txt

Output Set: N:\CRF4\02022005\J522106.raw

```

2290 His Lys Gly Val Ile Glu Met His Asn Tyr Cys Thr Ser Val Tyr Glu
2291      835      840      845
2292 Glu Gly Asp Ala Arg Ser Ala Leu Ile Thr Met Leu Gln Ser Leu His
2293      850      855      860
2294 His Ala Lys Asn Gly Val Asp Ile Val Ser Gly Thr Arg Val Lys Ser
2295 865      870      875      880
2296 His Phe Ala Lys Pro Asn Trp Arg Asn Val Tyr Lys Arg Ile Ala Leu
2297      885      890      895
2298 Asn His Pro Glu Ala Lys Val Gly Val Phe Tyr Cys Gly Ala Pro Ala
2299      900      905      910
2300 Leu Thr Lys Glu Leu Arg Gln His Ala Leu Asp Phe Ser His Lys Thr
2301      915      920      925
2302 Ser Thr Lys Phe Asp Phe His Lys Glu Asn Phe
2303      930      935

```

## VARIABLE LOCATION SUMMARY

DATE: 02/02/2005

PATENT APPLICATION: US/10/522,106

TIME: 15:31:43

Input Set : A:\Sequence Listing.txt

Output Set: N:\CRF4\02022005\J522106.raw,

Use of n's or Xaa's (NEW RULES):Use of n's and/or Xaa's have been detected in the Sequence Listing.Use of <220> to <223> is MANDATORY if n's or Xaa's are present.In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.

Seq#:1; Xaa Pos. 55 ✓

Seq#:2; Xaa Pos. 55 ✓

Seq#:15; N Pos. 1952 ✓

Seq#:15; Xaa Pos. 547 ✓

Seq#:16; Xaa Pos. 547 ✓

## VERIFICATION SUMMARY

DATE: 02/02/2005

PATENT APPLICATION: US/10/522,106

TIME: 15:31:43

Input Set : A:\Sequence Listing.txt

Output Set: N:\CRF4\02022005\J522106.raw

L:10 M:270 C: Current Application Number differs, Replaced Current Application Number  
L:15 M:283 W: Missing Blank Line separator, <210> field identifier  
L:19 M:283 W: Missing Blank Line separator, <220> field identifier  
L:23 M:283 W: Missing Blank Line separator, <400> field identifier  
L:34 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:1 after pos.:193  
L:49 M:283 W: Missing Blank Line separator, <400> field identifier  
L:56 M:340 E: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:2  
L:69 M:283 W: Missing Blank Line separator, <220> field identifier  
L:73 M:283 W: Missing Blank Line separator, <400> field identifier  
L:255 M:283 W: Missing Blank Line separator, <400> field identifier  
L:379 M:283 W: Missing Blank Line separator, <220> field identifier  
L:383 M:283 W: Missing Blank Line separator, <400> field identifier  
L:570 M:283 W: Missing Blank Line separator, <400> field identifier  
L:698 M:283 W: Missing Blank Line separator, <220> field identifier  
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L:1032 M:283 W: Missing Blank Line separator, <220> field identifier  
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L:1990 M:283 W: Missing Blank Line separator, <220> field identifier  
L:1994 M:283 W: Missing Blank Line separator, <400> field identifier  
L:2102 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:15 after pos.:1935  
M:341 Repeated in SeqNo=15  
L:2185 M:283 W: Missing Blank Line separator, <400> field identifier  
L:2254 M:340 E: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:16  
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L:3193 M:283 W: Missing Blank Line separator, <400> field identifier

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Legal Staff  
International Division

## SEQUENCE LISTING

<110> Kogel, Karl-Heinz  
Huckelhoven, Ralph  
Trujillo, Marco

<120> Method for Obtaining the pathogenic resistance in plants

<130> 12810-00067-US

<140> US 10/522,106

<141> 2005-01-24

<160> 24

<170> PatentIn version 3.3

<210> 1

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<212> DNA

<213> Hordeum vulgare

<220>

<221> CDS

<222> (2)..(337)

<223> coding for NADPH oxidase (fragment)

<400> 1

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  1             5             10            15
att gag atg cac aac tat ctc aca agt gtt tat gag gaa ggg gat gct 97
Ile Glu Met His Asn Tyr Leu Thr Ser Val Tyr Glu Glu Gly Asp Ala
      20             25             30
cgg tca gca ctc atc aca atg ctg caa gct ctc aac cat gcc aag aat 145
Arg Ser Ala Leu Ile Thr Met Leu Gln Ala Leu Asn His Ala Lys Asn
      35             40             45
ggg gtc gat gta gtg tct ggm act cga gtc cgg aca cat ttt gca aga 193
Gly Val Asp Val Val Ser Xaa Thr Arg Val Arg Thr His Phe Ala Arg
      50             55             60
cca aat ttt aag agg gtg ctg tct aag gta gcc gcc aaa cat cct tat 241
Pro Asn Phe Lys Arg Val Leu Ser Lys Val Ala Ala Lys His Pro Tyr
      65             70             75             80
gcc aag ata gga gtg ttc tat tgc gga gct cca gtt ctg gcg cag gaa 289
Ala Lys Ile Gly Val Phe Tyr Cys Gly Ala Pro Val Leu Ala Gln Glu
      85             90             95
cta agc aac ctt tgc cat gag ttc aat ggc aaa tgc acg aca aaa ttc 337
Leu Ser Asn Leu Cys His Glu Phe Asn Gly Lys Cys Thr Thr Lys Phe
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<210> 2

<211> 112

<212> PRT

<213> Hordeum vulgare

<220>

<221> misc\_feature

<222> (55)..(55)

<223> The 'Xaa' at location 55 stands for Gly.

<400> 2

Phe Lys Gly Ile Met Asn Glu Ile Ala Glu Leu Asp Gln Arg Asn Ile



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Ile	Glu	Met	His	Asn	Tyr	Leu	Thr	Ser	Val	Tyr	Glu	Glu	Gly	Asp	Ala	
			20					25					30			
Arg	Ser	Ala	Leu	Ile	Thr	Met	Leu	Gln	Ala	Leu	Asn	His	Ala	Lys	Asn	
		35					40					45				
Gly	Val	Asp	Val	Val	Ser	Xaa	Thr	Arg	Val	Arg	Thr	His	Phe	Ala	Arg	
	50					55					60					
Pro	Asn	Phe	Lys	Arg	Val	Leu	Ser	Lys	Val	Ala	Ala	Lys	His	Pro	Tyr	
	65				70					75					80	
Ala	Lys	Ile	Gly	Val	Phe	Tyr	Cys	Gly	Ala	Pro	Val	Leu	Ala	Gln	Glu	
			85					90						95		
Leu	Ser	Asn	Leu	Cys	His	Glu	Phe	Asn	Gly	Lys	Cys	Thr	Thr	Lys	Phe	
			100					105					110			

&lt;210&gt; 3

&lt;211&gt; 2832

&lt;212&gt; DNA

&lt;213&gt; Oryza sativa

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (1)..(2829)

&lt;223&gt; coding for NADPH oxidase

&lt;400&gt; 3

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Met	Arg	Gly	Gly	Ala	Ser	Ser	Gly	Pro	Gln	Arg	Trp	Gly	Ser	Ala	Gly	
1				5					10					15		
acg	aca	ccg	cgg	tcg	ctg	agc	acg	ggc	tcg	tcg	ccg	cgc	ggg	tcc	gac	96
Thr	Thr	Pro	Arg	Ser	Leu	Ser	Thr	Gly	Ser	Ser	Pro	Arg	Gly	Ser	Asp	
			20					25					30			
gac	cgg	agc	tcc	gac	gac	ggg	gag	ctg	gtc	gag	gtc	acg	ctc	gac		144
Asp	Arg	Ser	Ser	Asp	Asp	Gly	Glu	Leu	Val	Glu	Val	Thr	Leu	Asp		
		35				40					45					
ctg	cag	gac	gac	gac	acc	att	gtg	ctt	cgg	agc	gtc	gag	ccc	gcg	gcg	192
Leu	Gln	Asp	Asp	Asp	Thr	Ile	Val	Leu	Arg	Ser	Val	Glu	Pro	Ala	Ala	
	50					55					60					
gcg	gcg	gcg	gcg	ggg	gtg	ggg	gcg	ggg	gcg	ggg	gcg	gcg	tcg	gcg	cgg	240
Ala	Ala	Ala	Ala	Gly	Val	Gly	Ala	Gly	Ala	Gly	Ala	Ala	Ser	Ala	Arg	
	65			70				75						80		
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Gly	Glu	Leu	Thr	Gly	Gly	Pro	Ser	Ser	Ser	Ser	Ser	Arg	Ser	Arg	Ser	
			85					90						95		
cgg	tcg	atc	cgg	agg	agc	tcg	tcg	cac	cgg	ctg	ctg	cag	ttc	tcg	cag	336
Pro	Ser	Ile	Arg	Arg	Ser	Ser	Ser	His	Arg	Leu	Leu	Gln	Phe	Ser	Gln	
			100					105					110			
gag	ctc	aag	gcg	gag	gcc	atg	gcc	cgg	gcg	cgg	cag	ttc	tcg	cag	gac	384
Glu	Leu	Lys	Ala	Glu	Ala	Met	Ala	Arg	Ala	Arg	Gln	Phe	Ser	Gln	Asp	
		115				120						125				
ctg	acc	aag	cgg	ttc	ggc	cgc	agc	cac	agc	cgc	agc	gaa	gcg	cag	gcg	432
Leu	Thr	Lys	Arg	Phe	Gly	Arg	Ser	His	Ser	Arg	Ser	Glu	Ala	Gln	Ala	
	130				135							140				
cgg	tcg	ggc	ctc	gag	tcc	gcg	ctc	gcc	gcc	cgc	gcc	gcg	cgg	cgg	cag	480
Pro	Ser	Gly	Leu	Glu	Ser	Ala	Leu	Ala	Ala	Arg	Ala	Ala	Arg	Arg	Gln	
	145				150					155					160	
cgc	gcg	cag	ctc	gac	cgc	aca	cgc	tcc	ggc	gcc	cac	aag	gcg	ctc	cgc	528
Arg	Ala	Gln	Leu	Asp	Arg	Thr	Arg	Ser	Gly	Ala	His	Lys	Ala	Leu	Arg	
			165					170						175		
ggc	ctc	cgc	ttc	atc	agc	agc	aac	aag	gcc	aac	aac	gcc	tgg	atg	gag	576
Gly	Leu	Arg	Phe	Ile	Ser	Ser	Asn	Lys	Ala	Asn	Asn	Ala	Trp	Met	Glu	
			180					185					190			

gtg	cag	gcc	aac	ttc	gac	cgc	ctc	gcc	cgc	gac	ggc	tac	ctc	tcc	cgc	624
Val	Gln	Ala	Asn	Phe	Asp	Arg	Leu	Ala	Arg	Asp	Gly	Tyr	Leu	Ser	Arg	
		195					200					205				
tcc	gac	ttc	gcc	gaa	tgc	atc	ggg	atg	acg	gaa	tcg	aag	gag	ttc	gcg	672
Ser	Asp	Phe	Ala	Glu	Cys	Ile	Gly	Met	Thr	Glu	Ser	Lys	Glu	Phe	Ala	
	210					215					220					
ctc	gag	ctg	ttc	gac	acg	ctg	agc	cgg	cga	cga	cag	atg	aag	gtg	gac	720
Leu	Glu	Leu	Phe	Asp	Thr	Leu	Ser	Arg	Arg	Arg	Gln	Met	Lys	Val	Asp	
	225				230					235					240	
acg	att	aac	aag	gat	gaa	ctc	cgc	gag	atc	tgg	cag	cag	atc	acc	gat	768
Thr	Ile	Asn	Lys	Asp	Glu	Leu	Arg	Glu	Ile	Trp	Gln	Gln	Ile	Thr	Asp	
				245					250					255		
aac	agc	ttc	gac	tcc	cgt	ctc	caa	atc	ttc	ttc	gaa	atg	gtg	gat	aag	816
Asn	Ser	Phe	Asp	Ser	Arg	Leu	Gln	Ile	Phe	Phe	Glu	Met	Val	Asp	Lys	
			260					265					270			
aac	gcg	gac	ggc	cgg	att	acg	gag	gcg	gag	gtg	aaa	gag	att	att	atg	864
Asn	Ala	Asp	Gly	Arg	Ile	Thr	Glu	Ala	Glu	Val	Lys	Glu	Ile	Ile	Met	
		275					280					285				
ttg	agc	gcg	tct	gcc	aat	aaa	ctg	tcg	agg	ctt	aag	gag	caa	gca	gaa	912
Leu	Ser	Ala	Ser	Ala	Asn	Lys	Leu	Ser	Arg	Leu	Lys	Glu	Gln	Ala	Glu	
	290					295					300					
gag	tac	gcc	gct	ttg	atc	atg	gag	gag	ctt	gat	cct	gaa	ggg	ctc	ggc	960
Glu	Tyr	Ala	Ala	Leu	Ile	Met	Glu	Glu	Leu	Asp	Pro	Glu	Gly	Leu	Gly	
	305				310					315					320	
tac	att	gag	cta	tgg	caa	ttg	gag	aca	ctt	ctg	ttg	cag	aaa	gat	acc	1008
Tyr	Ile	Glu	Leu	Trp	Gln	Leu	Glu	Thr	Leu	Leu	Leu	Gln	Lys	Asp	Thr	
			325						330					335		
tat	atg	aac	tat	agt	cag	gcc	ctt	agt	tac	aca	agc	caa	gca	ctg	agc	1056
Tyr	Met	Asn	Tyr	Ser	Gln	Ala	Leu	Ser	Tyr	Thr	Ser	Gln	Ala	Leu	Ser	
			340					345					350			
cag	aat	ctt	gca	ggg	cta	agg	aag	aag	agt	tca	atc	cgc	aaa	ata	agc	1104
Gln	Asn	Leu	Ala	Gly	Leu	Arg	Lys	Lys	Ser	Ser	Ile	Arg	Lys	Ile	Ser	
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Thr	Ser	Leu	Ser	Tyr	Tyr	Phe	Glu	Asp	Asn	Trp	Lys	Arg	Leu	Trp	Val	
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ctt	gca	ttg	tgg	att	ggg	ata	atg	gct	gga	ctg	ttc	acc	tgg	aaa	ttc	1200
Leu	Ala	Leu	Trp	Ile	Gly	Ile	Met	Ala	Gly	Leu	Phe	Thr	Trp	Lys	Phe	
	385				390					395					400	
atg	cag	tat	cgt	aac	cga	tat	gtc	ttt	gat	gtg	atg	ggc	tac	tgt	gtc	1248
Met	Gln	Tyr	Arg	Asn	Arg	Tyr	Val	Phe	Asp	Val	Met	Gly	Tyr	Cys	Val	
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aca	aca	gca	aaa	gga	gct	gct	gaa	acc	cta	aag	ctg	aat	atg	gca	att	1296
Thr	Thr	Ala	Lys	Gly	Ala	Ala	Glu	Thr	Leu	Lys	Leu	Asn	Met	Ala	Ile	
			420					425					430			
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Ile	Leu	Leu	Pro	Val	Cys	Arg	Asn	Thr	Ile	Thr	Trp	Leu	Arg	Ser	Thr	
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agg	gct	gca	cgg	gca	cta	cct	ttt	gat	gac	aac	atc	aac	ttc	cac	aag	1392
Arg	Ala	Ala	Arg	Ala	Leu	Pro	Phe	Asp	Asp	Asn	Ile	Asn	Phe	His	Lys	
		450				455					460					
act	att	gca	gca	gca	att	gtg	ggt	ggt	ata	atc	ctc	cat	gca	ggg	aac	1440
Thr	Ile	Ala	Ala	Ala	Ile	Val	Val	Gly	Ile	Ile	Leu	His	Ala	Gly	Asn	
	465				470					475					480	
cac	ctt	gta	tgc	gat	ttt	cca	cgg	tta	ata	aaa	tca	tca	gat	gag	aag	1488
His	Leu	Val	Cys	Asp	Phe	Pro	Arg	Leu	Ile	Lys	Ser	Ser	Asp	Glu	Lys	
				485					490					495		
tat	gct	cct	ttg	ggc	cag	tat	ttt	ggg	gaa	ata	aag	cca	aca	tat	ttt	1536
Tyr	Ala	Pro	Leu	Gly	Gln	Tyr	Phe	Gly	Glu	Ile	Lys	Pro	Thr	Tyr	Phe	
			500					505					510			
aca	ttg	gtc	aaa	gga	gtg	gag	ggc	atc	act	ggg	gta	atc	atg	ggt	gta	1584

Thr	Leu	Val	Lys	Gly	Val	Glu	Gly	Ile	Thr	Gly	Val	Ile	Met	Val	Val	
		515					520					525				
tgc	atg	ata	att	gct	ttt	act	cta	gca	acc	cgg	tgg	ttc	cgc	cgt	agc	1632
Cys	Met	Ile	Ile	Ala	Phe	Thr	Leu	Ala	Thr	Arg	Trp	Phe	Arg	Arg	Ser	
		530					535					540				
ttg	ggt	aag	ctt	cca	agg	cca	ttt	gac	aaa	ctg	act	ggc	ttc	aat	gcc	1680
Leu	Val	Lys	Leu	Pro	Arg	Pro	Phe	Asp	Lys	Leu	Thr	Gly	Phe	Asn	Ala	
		545			550						555				560	
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Phe	Trp	Tyr	Ser	His	His	Leu	Phe	Ile	Ile	Val	Tyr	Ile	Ala	Leu	Ile	
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ggt	cat	gga	gag	tgt	cta	tac	ctt	att	cat	gtc	tgg	tac	aga	aga	acg	1776
Val	His	Gly	Glu	Cys	Leu	Tyr	Leu	Ile	His	Val	Trp	Tyr	Arg	Arg	Thr	
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aca	tgg	atg	tat	ctt	tca	gtg	cct	ggt	tgc	ttg	tat	gta	ggg	gag	agg	1824
Thr	Trp	Met	Tyr	Leu	Ser	Val	Pro	Val	Cys	Leu	Tyr	Val	Gly	Glu	Arg	
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Pro	Thr	Phe	Arg	Tyr	Lys	Ser	Gly	Gln	Tyr	Met	Phe	Val	Gln	Cys	Pro	
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Ala	Val	Ser	Pro	Phe	Glu	Trp	His	Pro	Phe	Ser	Ile	Thr	Ser	Ala	Pro	
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Gly	Asp	Asp	Tyr	Leu	Ser	Ile	His	Val	Arg	Gln	Leu	Gly	Asp	Trp	Thr	
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Arg	Glu	Leu	Lys	Arg	Val	Phe	Ala	Ala	Ala	Cys	Glu	Pro	Pro	Ala	Gly	
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ccc	aag	ctt	ctg	att	gat	gga	cgg	tat	ggt	tct	cct	gct	cag	gat	tac	2208
Pro	Lys	Leu	Leu	Ile	Asp	Gly	Pro	Tyr	Gly	Ser	Pro	Ala	Gln	Asp	Tyr	
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Ser	Lys	Tyr	Asp	Val	Leu	Leu	Leu	Val	Gly	Leu	Gly	Ile	Gly	Ala	Thr	
			740						745					750		
ccc	ttt	att	agc	ata	tta	aaa	gat	ctt	ctg	aat	aac	atc	atc	aaa	atg	2304
Pro	Phe	Ile	Ser	Ile	Leu	Lys	Asp	Leu	Leu	Asn	Asn	Ile	Ile	Lys	Met	
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gag	gaa	gag	gag	gat	gct	tct	act	gat	ctt	tat	cca	cca	atg	ggt	cgg	2352
Glu	Glu	Glu	Glu	Asp	Ala	Ser	Thr	Asp	Leu	Tyr	Pro	Pro	Met	Gly	Arg	
		770					775					780				
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Asn	Lys	Pro	His	Val	Asp	Leu	Gly	Thr	Leu	Met	Thr	Ile	Thr	Ser	Arg	
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Pro	Lys	Lys	Ile	Leu	Lys	Thr	Thr	Asn	Ala	Tyr	Phe	Tyr	Trp	Val	Thr	
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cgt	gag	caa	ggc	tct	ttt	gat	tgg	ttc	aaa	gga	gtc	atg	aat	gaa	att	2496
Arg	Glu	Gln	Gly	Ser	Phe	Asp	Trp	Phe	Lys	Gly	Val	Met	Asn	Glu	Ile	
			820					825						830		
gct	gac	ttg	gat	caa	agg	aat	atc	att	gag	atg	cac	aac	tac	cta	aca	2544
Ala	Asp	Leu	Asp	Gln	Arg	Asn	Ile	Ile	Glu	Met	His	Asn	Tyr	Leu	Thr	

835	840	845	
agc gtc tat gag gag ggg gat gcc agg tca gca ctc atc acc atg ctc			2592
Ser Val Tyr Glu Glu Gly Asp Ala Arg Ser Ala Leu Ile Thr Met Leu			
850	855	860	
caa gct ctg aac cat gcc aag aat gga gtt gat att gtc tct ggg aca			2640
Gln Ala Leu Asn His Ala Lys Asn Gly Val Asp Ile Val Ser Gly Thr			
865	870	875	880
aaa gtc cgg aca cat ttt gca cga cca aat tgg aga aag gtc ctt tct			2688
Lys Val Arg Thr His Phe Ala Arg Pro Asn Trp Arg Lys Val Leu Ser			
	885	890	895
aaa att tcc tcc aag cat cca tat gcc aaa ata ggt gta ttc tac tgt			2736
Lys Ile Ser Ser Lys His Pro Tyr Ala Lys Ile Gly Val Phe Tyr Cys			
	900	905	910
gga gct cca gtc ctg gca caa gaa cta agc aaa ctt tgc cat gaa ttc			2784
Gly Ala Pro Val Leu Ala Gln Glu Leu Ser Lys Leu Cys His Glu Phe			
	915	920	925
aac ggg aaa tgc aca acg aag ttc gaa ttc cat aag gag cat ttc tga			2832
Asn Gly Lys Cys Thr Thr Lys Phe Glu Phe His Lys Glu His Phe			
930	935	940	

&lt;210&gt; 4

&lt;211&gt; 943

&lt;212&gt; PRT

&lt;213&gt; Oryza sativa

&lt;400&gt; 4

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Thr Thr Pro Arg Ser Leu Ser Thr Gly Ser Ser Pro Arg Gly Ser Asp	
20 25 30	
Asp Arg Ser Ser Asp Asp Gly Glu Leu Val Glu Val Thr Leu Asp	
35 40 45	
Leu Gln Asp Asp Asp Thr Ile Val Leu Arg Ser Val Glu Pro Ala Ala	
50 55 60	
Ala Ala Ala Ala Gly Val Gly Ala Gly Ala Gly Ala Ala Ser Ala Arg	
65 70 75 80	
Gly Glu Leu Thr Gly Gly Pro Ser Ser Ser Ser Ser Arg Ser Arg Ser	
85 90 95	
Pro Ser Ile Arg Arg Ser Ser Ser His Arg Leu Leu Gln Phe Ser Gln	
100 105 110	
Glu Leu Lys Ala Glu Ala Met Ala Arg Ala Arg Gln Phe Ser Gln Asp	
115 120 125	
Leu Thr Lys Arg Phe Gly Arg Ser His Ser Arg Ser Glu Ala Gln Ala	
130 135 140	
Pro Ser Gly Leu Glu Ser Ala Leu Ala Ala Arg Ala Ala Arg Arg Gln	
145 150 155 160	
Arg Ala Gln Leu Asp Arg Thr Arg Ser Gly Ala His Lys Ala Leu Arg	
165 170 175	
Gly Leu Arg Phe Ile Ser Ser Asn Lys Ala Asn Asn Ala Trp Met Glu	
180 185 190	
Val Gln Ala Asn Phe Asp Arg Leu Ala Arg Asp Gly Tyr Leu Ser Arg	
195 200 205	
Ser Asp Phe Ala Glu Cys Ile Gly Met Thr Glu Ser Lys Glu Phe Ala	
210 215 220	
Leu Glu Leu Phe Asp Thr Leu Ser Arg Arg Arg Gln Met Lys Val Asp	
225 230 235 240	
Thr Ile Asn Lys Asp Glu Leu Arg Glu Ile Trp Gln Gln Ile Thr Asp	
245 250 255	
Asn Ser Phe Asp Ser Arg Leu Gln Ile Phe Phe Glu Met Val Asp Lys	
260 265 270	
Asn Ala Asp Gly Arg Ile Thr Glu Ala Glu Val Lys Glu Ile Ile Met	

		275				280				285					
Leu	Ser	Ala	Ser	Ala	Asn	Lys	Leu	Ser	Arg	Leu	Lys	Glu	Gln	Ala	Glu
	290					295					300				
Glu	Tyr	Ala	Ala	Leu	Ile	Met	Glu	Glu	Leu	Asp	Pro	Glu	Gly	Leu	Gly
305					310					315					320
Tyr	Ile	Glu	Leu	Trp	Gln	Leu	Glu	Thr	Leu	Leu	Leu	Gln	Lys	Asp	Thr
				325					330					335	
Tyr	Met	Asn	Tyr	Ser	Gln	Ala	Leu	Ser	Tyr	Thr	Ser	Gln	Ala	Leu	Ser
			340					345					350		
Gln	Asn	Leu	Ala	Gly	Leu	Arg	Lys	Lys	Ser	Ser	Ile	Arg	Lys	Ile	Ser
	355						360					365			
Thr	Ser	Leu	Ser	Tyr	Tyr	Phe	Glu	Asp	Asn	Trp	Lys	Arg	Leu	Trp	Val
	370					375					380				
Leu	Ala	Leu	Trp	Ile	Gly	Ile	Met	Ala	Gly	Leu	Phe	Thr	Trp	Lys	Phe
385					390					395					400
Met	Gln	Tyr	Arg	Asn	Arg	Tyr	Val	Phe	Asp	Val	Met	Gly	Tyr	Cys	Val
				405					410					415	
Thr	Thr	Ala	Lys	Gly	Ala	Ala	Glu	Thr	Leu	Lys	Leu	Asn	Met	Ala	Ile
			420					425					430		
Ile	Leu	Leu	Pro	Val	Cys	Arg	Asn	Thr	Ile	Thr	Trp	Leu	Arg	Ser	Thr
	435						440					445			
Arg	Ala	Ala	Arg	Ala	Leu	Pro	Phe	Asp	Asp	Asn	Ile	Asn	Phe	His	Lys
	450					455					460				
Thr	Ile	Ala	Ala	Ala	Ile	Val	Val	Gly	Ile	Ile	Leu	His	Ala	Gly	Asn
465					470					475					480
His	Leu	Val	Cys	Asp	Phe	Pro	Arg	Leu	Ile	Lys	Ser	Ser	Asp	Glu	Lys
			485						490					495	
Tyr	Ala	Pro	Leu	Gly	Gln	Tyr	Phe	Gly	Glu	Ile	Lys	Pro	Thr	Tyr	Phe
			500					505					510		
Thr	Leu	Val	Lys	Gly	Val	Glu	Gly	Ile	Thr	Gly	Val	Ile	Met	Val	Val
	515						520					525			
Cys	Met	Ile	Ile	Ala	Phe	Thr	Leu	Ala	Thr	Arg	Trp	Phe	Arg	Arg	Ser
	530					535					540				
Leu	Val	Lys	Leu	Pro	Arg	Pro	Phe	Asp	Lys	Leu	Thr	Gly	Phe	Asn	Ala
545					550					555					560
Phe	Trp	Tyr	Ser	His	His	Leu	Phe	Ile	Ile	Val	Tyr	Ile	Ala	Leu	Ile
			565						570					575	
Val	His	Gly	Glu	Cys	Leu	Tyr	Leu	Ile	His	Val	Trp	Tyr	Arg	Arg	Thr
			580					585					590		
Thr	Trp	Met	Tyr	Leu	Ser	Val	Pro	Val	Cys	Leu	Tyr	Val	Gly	Glu	Arg
	595						600					605			
Ile	Leu	Arg	Phe	Phe	Arg	Ser	Gly	Ser	Tyr	Ser	Val	Arg	Leu	Leu	Lys
	610					615					620				
Val	Ala	Ile	Tyr	Pro	Gly	Asn	Val	Leu	Thr	Leu	Gln	Met	Ser	Lys	Pro
625					630					635					640
Pro	Thr	Phe	Arg	Tyr	Lys	Ser	Gly	Gln	Tyr	Met	Phe	Val	Gln	Cys	Pro
			645						650					655	
Ala	Val	Ser	Pro	Phe	Glu	Trp	His	Pro	Phe	Ser	Ile	Thr	Ser	Ala	Pro
			660					665					670		
Gly	Asp	Asp	Tyr	Leu	Ser	Ile	His	Val	Arg	Gln	Leu	Gly	Asp	Trp	Thr
	675					680						685			
Arg	Glu	Leu	Lys	Arg	Val	Phe	Ala	Ala	Ala	Cys	Glu	Pro	Pro	Ala	Gly
	690					695					700				
Gly	Lys	Ser	Gly	Leu	Leu	Arg	Ala	Asp	Glu	Thr	Thr	Lys	Lys	Ile	Leu
705					710					715					720
Pro	Lys	Leu	Leu	Ile	Asp	Gly	Pro	Tyr	Gly	Ser	Pro	Ala	Gln	Asp	Tyr
				725					730					735	
Ser	Lys	Tyr	Asp	Val	Leu	Leu	Leu	Val	Gly	Leu	Gly	Ile	Gly	Ala	Thr
			740					745					750		
Pro	Phe	Ile	Ser	Ile	Leu	Lys	Asp	Leu	Leu	Asn	Asn	Ile	Ile	Lys	Met
	755						760					765			

Glu	Glu	Glu	Glu	Asp	Ala	Ser	Thr	Asp	Leu	Tyr	Pro	Pro	Met	Gly	Arg	
770						775					780					
Asn	Lys	Pro	His	Val	Asp	Leu	Gly	Thr	Leu	Met	Thr	Ile	Thr	Ser	Arg	
785					790					795					800	
Pro	Lys	Lys	Ile	Leu	Lys	Thr	Thr	Asn	Ala	Tyr	Phe	Tyr	Trp	Val	Thr	
				805					810					815		
Arg	Glu	Gln	Gly	Ser	Phe	Asp	Trp	Phe	Lys	Gly	Val	Met	Asn	Glu	Ile	
			820					825					830			
Ala	Asp	Leu	Asp	Gln	Arg	Asn	Ile	Ile	Glu	Met	His	Asn	Tyr	Leu	Thr	
			835				840					845				
Ser	Val	Tyr	Glu	Glu	Gly	Asp	Ala	Arg	Ser	Ala	Leu	Ile	Thr	Met	Leu	
	850					855					860					
Gln	Ala	Leu	Asn	His	Ala	Lys	Asn	Gly	Val	Asp	Ile	Val	Ser	Gly	Thr	
865					870					875					880	
Lys	Val	Arg	Thr	His	Phe	Ala	Arg	Pro	Asn	Trp	Arg	Lys	Val	Leu	Ser	
				885					890					895		
Lys	Ile	Ser	Ser	Lys	His	Pro	Tyr	Ala	Lys	Ile	Gly	Val	Phe	Tyr	Cys	
			900					905					910			
Gly	Ala	Pro	Val	Leu	Ala	Gln	Glu	Leu	Ser	Lys	Leu	Cys	His	Glu	Phe	
		915					920					925				
Asn	Gly	Lys	Cys	Thr	Thr	Lys	Phe	Glu	Phe	His	Lys	Glu	His	Phe		
	930					935					940					

&lt;210&gt; 5

&lt;211&gt; 2889

&lt;212&gt; DNA

&lt;213&gt; Nicotiana tabacum

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (1)..(2886)

&lt;223&gt; coding for NADPH oxidase

&lt;400&gt; 5

atg	agg	ggt	tta	cct	ggg	cat	gaa	cgc	cgg	tgg	aca	tcc	gat	acg	gta	48
Met	Arg	Gly	Leu	Pro	Gly	His	Glu	Arg	Arg	Trp	Thr	Ser	Asp	Thr	Val	
1				5					10					15		
tct	tcc	gac	aag	gat	ttt	agt	ggt	gaa	tta	tcg	ccg	gga	gct	gat	tcc	96
Ser	Ser	Asp	Lys	Asp	Phe	Ser	Gly	Glu	Leu	Ser	Pro	Gly	Ala	Asp	Ser	
			20					25					30			
ggc	tat	aat	tcc	ggt	ttt	gct	tcc	gag	gag	ttt	ggt	gaa	gtc	acg	ctt	144
Gly	Tyr	Asn	Ser	Gly	Phe	Ala	Ser	Glu	Glu	Phe	Val	Glu	Val	Thr	Leu	
		35					40					45				
gat	ctt	cag	gat	gat	gat	acc	att	att	cta	cgg	agc	ggt	gaa	ccg	gct	192
Asp	Leu	Gln	Asp	Asp	Asp	Thr	Ile	Ile	Leu	Arg	Ser	Val	Glu	Pro	Ala	
	50					55				60						
act	gtg	att	aac	att	gac	gct	cct	gat	ctt	ccc	gcc	gga	gtc	ggt	att	240
Thr	Val	Ile	Asn	Ile	Asp	Ala	Pro	Asp	Leu	Pro	Ala	Gly	Val	Gly	Ile	
	65				70				75					80		
tcc	gga	ggt	tca	att	gaa	act	ccg	acg	tca	gca	tcg	gtg	tcg	gaa	tct	288
Ser	Gly	Val	Ser	Ile	Glu	Thr	Pro	Thr	Ser	Ala	Ser	Val	Ser	Glu	Ser	
				85					90					95		
cga	tcg	ccg	acg	atc	cgc	cgg	agt	tca	tct	agt	aaa	ctt	cgt	cag	ttt	336
Arg	Ser	Pro	Thr	Ile	Arg	Arg	Ser	Ser	Ser	Ser	Lys	Leu	Arg	Gln	Phe	
			100					105					110			
tca	cag	gag	ttg	aaa	gct	gag	gcg	ggt	gcg	aaa	gcg	agg	cag	ttt	tca	384
Ser	Gln	Glu	Leu	Lys	Ala	Glu	Ala	Val	Ala	Lys	Ala	Arg	Gln	Phe	Ser	
		115					120					125				
caa	gag	ctg	aag	gcg	gag	tta	agg	aga	ttc	tca	tgg	agc	cat	ggg	cat	432
Gln	Glu	Leu	Lys	Ala	Glu	Leu	Arg	Arg	Phe	Ser	Trp	Ser	His	Gly	His	
	130					135					140					

gcg	tct	cgc	gcg	ttt	tcg	ccc	tcg	tcg	ttt	ttt	caa	aac	gcc	gtc	gtt	480
Ala	Ser	Arg	Ala	Phe	Ser	Pro	Ser	Ser	Phe	Phe	Gln	Asn	Ala	Val	Val	
145					150					155					160	
gga	aca	ggt	aac	ggc	gtg	gac	tcg	gct	tta	gcg	gca	cgt	gca	tta	cgt	528
Gly	Thr	Gly	Asn	Gly	Val	Asp	Ser	Ala	Leu	Ala	Ala	Arg	Ala	Leu	Arg	
				165					170					175		
cgg	caa	cgc	gcg	cag	ctt	gat	cgg	act	cgt	tcc	agc	gcc	cat	aga	gct	576
Arg	Gln	Arg	Ala	Gln	Leu	Asp	Arg	Thr	Arg	Ser	Ser	Ala	His	Arg	Ala	
			180					185				190				
ctt	cgt	aga	ctc	aaa	ttc	att	agc	aat	aac	aaa	acc	aat	gga	tgg	aat	624
Leu	Arg	Arg	Leu	Lys	Phe	Ile	Ser	Asn	Asn	Lys	Thr	Asn	Gly	Trp	Asn	
		195					200				205					
gaa	gtt	gaa	aac	aat	ttc	tca	aag	ctc	gct	aaa	gac	ggg	tat	ctt	tac	672
Glu	Val	Glu	Asn	Asn	Phe	Ser	Lys	Leu	Ala	Lys	Asp	Gly	Tyr	Leu	Tyr	
	210					215					220					
cgt	tcc	gat	ttc	gca	caa	tgc	ata	ggg	atg	aag	gat	tcg	aag	gaa	ttt	720
Arg	Ser	Asp	Phe	Ala	Gln	Cys	Ile	Gly	Met	Lys	Asp	Ser	Lys	Glu	Phe	
225				230						235					240	
gca	ttg	gaa	tta	ttt	gat	gct	ttg	agt	aga	aga	aga	aga	tta	aag	gtt	768
Ala	Leu	Glu	Leu	Phe	Asp	Ala	Leu	Ser	Arg	Arg	Arg	Arg	Leu	Lys	Val	
				245					250					255		
gat	aaa	att	agc	aag	gag	gaa	ttg	tat	gag	tac	tgg	tct	caa	atc	acc	816
Asp	Lys	Ile	Ser	Lys	Glu	Glu	Leu	Tyr	Glu	Tyr	Trp	Ser	Gln	Ile	Thr	
			260					265					270			
gat	cag	agt	ttc	gat	tct	cgg	ctt	cag	atc	tcc	ttc	gac	atg	gtg	gac	864
Asp	Gln	Ser	Phe	Asp	Ser	Arg	Leu	Gln	Ile	Ser	Phe	Asp	Met	Val	Asp	
		275					280					285				
aag	aat	gaa	gat	ggg	cga	att	gct	gaa	gag	gaa	gta	aaa	gag	atc	atc	912
Lys	Asn	Glu	Asp	Gly	Arg	Ile	Ala	Glu	Glu	Glu	Val	Lys	Glu	Ile	Ile	
	290					295					300					
atg	cta	agt	gca	tct	gca	aac	aag	tta	tca	aga	tta	aaa	gaa	caa	gca	960
Met	Leu	Ser	Ala	Ser	Ala	Asn	Lys	Leu	Ser	Arg	Leu	Lys	Glu	Gln	Ala	
305					310					315					320	
gag	gag	tat	gca	gct	tta	atc	atg	gaa	gaa	tta	gat	cct	gaa	aga	ctc	1008
Glu	Glu	Tyr	Ala	Ala	Leu	Ile	Met	Glu	Glu	Leu	Asp	Pro	Glu	Arg	Leu	
			325					330						335		
ggc	tac	att	gag	cta	tgg	cag	ctg	gaa	aca	ctt	ctc	ctc	caa	aag	gac	1056
Gly	Tyr	Ile	Glu	Leu	Trp	Gln	Leu	Glu	Thr	Leu	Leu	Leu	Gln	Lys	Asp	
			340					345					350			
act	tac	ctc	aac	tac	agt	caa	gca	cta	agt	tac	acg	agc	caa	gcc	ttg	1104
Thr	Tyr	Leu	Asn	Tyr	Ser	Gln	Ala	Leu	Ser	Tyr	Thr	Ser	Gln	Ala	Leu	
		355					360					365				
agc	caa	aac	ctt	cac	gga	tta	agg	aag	aaa	agc	cca	ata	aaa	aga	atg	1152
Ser	Gln	Asn	Leu	His	Gly	Leu	Arg	Lys	Lys	Ser	Pro	Ile	Lys	Arg	Met	
	370					375					380					
agc	aca	aaa	ctt	gtc	tat	tca	ttg	caa	gaa	aac	tgg	aag	aga	att	tgg	1200
Ser	Thr	Lys	Leu	Val	Tyr	Ser	Leu	Gln	Glu	Asn	Trp	Lys	Arg	Ile	Trp	
385				390						395					400	
gtt	ctc	act	tta	tgg	att	ttg	ata	atg	att	ggg	ctt	ttt	ctt	tgg	aag	1248
Val	Leu	Thr	Leu	Trp	Ile	Leu	Ile	Met	Ile	Gly	Leu	Phe	Leu	Trp	Lys	
			405						410					415		
ttc	tat	cag	tac	aaa	aac	aag	agt	gca	ttc	cgt	gtc	atg	ggg	tat	tgc	1296
Phe	Tyr	Gln	Tyr	Lys	Asn	Lys	Ser	Ala	Phe	Arg	Val	Met	Gly	Tyr	Cys	
			420					425					430			
ctt	gtc	acg	gct	aag	ggc	gct	gct	gag	act	ctc	aag	ttc	aac	atg	gct	1344
Leu	Val	Thr	Ala	Lys	Gly	Ala	Ala	Glu	Thr	Leu	Lys	Phe	Asn	Met	Ala	
		435				440						445				
ctt	ata	tta	ttg	cca	gta	tgc	aga	aac	act	att	aca	tgg	ctc	agg	tcc	1392
Leu	Ile	Leu	Leu	Pro	Val	Cys	Arg	Asn	Thr	Ile	Thr	Trp	Leu	Arg	Ser	
	450					455					460					
acc	aag	ttg	agc	cat	ttt	gta	ccc	ttt	gac	gac	aac	atc	aac	ttt	cac	1440

Thr 465	Lys	Leu	Ser	His	Phe 470	Val	Pro	Phe	Asp	Asp 475	Asn	Ile	Asn	Phe	His 480	
aag	act	gtc	gct	gca	gcc	att	gtc	act	ggg	atc	ata	ctc	cat	gct	ggg	1488
Lys	Thr	Val	Ala	Ala	Ala	Ile	Val	Thr	Gly	Ile	Ile	Leu	His	Ala	Gly	
					485				490					495		
aac	cat	ctt	gta	tgt	gat	ttc	cca	agg	ctt	ata	cat	gca	gat	gat	caa	1536
Asn	His	Leu	Val	Cys	Asp	Phe	Pro	Arg	Leu	Ile	His	Ala	Asp	Asp	Gln	
			500					505				510				
gat	tat	caa	agt	ttt	ttg	tcg	aat	gat	ttt	ggc	caa	agt	aag	cct	gga	1584
Asp	Tyr	Gln	Ser	Phe	Leu	Ser	Asn	Asp	Phe	Gly	Gln	Ser	Lys	Pro	Gly	
		515					520					525				
tac	ata	gac	ctt	gtt	aaa	gga	gtt	gag	ggg	gtg	acg	gga	ata	ata	atg	1632
Tyr	Ile	Asp	Leu	Val	Lys	Gly	Val	Glu	Gly	Val	Thr	Gly	Ile	Ile	Met	
		530				535						540				
gta	atc	ctt	atg	gcc	att	gct	ttc	act	ctt	gct	aca	cga	tgg	ttt	aga	1680
Val	Ile	Leu	Met	Ala	Ile	Ala	Phe	Thr	Leu	Ala	Thr	Arg	Trp	Phe	Arg	
					550					555					560	
cgg	agc	ctc	att	aag	ttg	ccc	aaa	cct	ttt	gat	aga	ctc	act	ggc	ttc	1728
Arg	Ser	Leu	Ile	Lys	Leu	Pro	Lys	Pro	Phe	Asp	Arg	Leu	Thr	Gly	Phe	
				565					570					575		
aat	gca	ttc	tgg	tat	tca	cac	cac	ctt	ctt	gtc	att	gtc	tac	atc	cta	1776
Asn	Ala	Phe	Trp	Tyr	Ser	His	His	Leu	Leu	Val	Ile	Val	Tyr	Ile	Leu	
			580					585					590			
ctg	atc	atc	cat	ggc	acg	ttc	ctc	ttc	ctt	gtg	cat	aaa	tgg	tac	tcc	1824
Leu	Ile	Ile	His	Gly	Thr	Phe	Leu	Phe	Leu	Val	His	Lys	Trp	Tyr	Ser	
			595				600					605				
aag	acg	acg	tgg	atg	tat	cta	gca	gtt	cct	gtg	ctt	ctc	tac	gca	ggg	1872
Lys	Thr	Thr	Trp	Met	Tyr	Leu	Ala	Val	Pro	Val	Leu	Leu	Tyr	Ala	Gly	
		610				615					620					
gaa	aga	act	ctt	aga	ttc	ttc	cgg	tca	ggc	ttg	tac	act	gtc	cgg	ctt	1920
Glu	Arg	Thr	Leu	Arg	Phe	Phe	Arg	Ser	Gly	Leu	Tyr	Thr	Val	Arg	Leu	
					630				635						640	
ctg	aaa	gta	gca	ata	tat	cct	gga	aat	gtc	ctc	act	cta	caa	atg	tct	1968
Leu	Lys	Val	Ala	Ile	Tyr	Pro	Gly	Asn	Val	Leu	Thr	Leu	Gln	Met	Ser	
				645				650						655		
aag	cct	cct	caa	ttt	cga	tac	aaa	agt	gga	caa	tat	atg	ttt	gtc	cag	2016
Lys	Pro	Pro	Gln	Phe	Arg	Tyr	Lys	Ser	Gly	Gln	Tyr	Met	Phe	Val	Gln	
			660					665				670				
tgt	cca	gct	gtt	tct	cca	ttc	gag	tgg	cat	cca	ttt	tcc	att	act	tca	2064
Cys	Pro	Ala	Val	Ser	Pro	Phe	Glu	Trp	His	Pro	Phe	Ser	Ile	Thr	Ser	
		675					680					685				
gct	cct	ggg	gat	gac	tac	ttg	agc	att	cac	atc	cgg	caa	ctt	ggg	gac	2112
Ala	Pro	Gly	Asp	Asp	Tyr	Leu	Ser	Ile	His	Ile	Arg	Gln	Leu	Gly	Asp	
		690				695					700					
tgg	act	caa	gaa	ctc	aag	cgg	gtc	ttt	tct	gag	gct	tgc	gag	cgg	cca	2160
Trp	Thr	Gln	Glu	Leu	Lys	Arg	Val	Phe	Ser	Glu	Ala	Cys	Glu	Arg	Pro	
					710					715					720	
gag	gct	gga	aag	agt	ggc	ctg	ctc	aga	gct	gac	gaa	aac	act	aag	aaa	2208
Glu	Ala	Gly	Lys	Ser	Gly	Leu	Leu	Arg	Ala	Asp	Glu	Asn	Thr	Lys	Lys	
				725					730					735		
agt	ttg	cca	aag	cta	tta	ata	gat	gga	cct	tac	gga	gct	cca	gca	caa	2256
Ser	Leu	Pro	Lys	Leu	Leu	Ile	Asp	Gly	Pro	Tyr	Gly	Ala	Pro	Ala	Gln	
			740					745					750			
gat	tac	cga	aaa	tat	gat	gtc	ttg	ctg	ctt	gtt	ggg	ctt	ggc	att	gga	2304
Asp	Tyr	Arg	Lys	Tyr	Asp	Val	Leu	Leu	Leu	Val	Gly	Leu	Gly	Ile	Gly	
			755			760						765				
gca	acg	ccg	ttc	ata	agt	atc	ctg	aaa	gac	ttg	ctc	gtt	aac	atc	gtg	2352
Ala	Thr	Pro	Phe	Ile	Ser	Ile	Leu	Lys	Asp	Leu	Leu	Val	Asn	Ile	Val	
			770			775					780					
aaa	atg	gag	gag	caa	gca	gat	tta	gcc	tca	gat	ttc	agt	ggg	aac	tca	2400
Lys	Met	Glu	Glu	Gln	Ala	Asp	Leu	Ala	Ser	Asp	Phe	Ser	Gly	Asn	Ser	



785		790		795		800	
gac atg agc gtt gcg aca agt gaa caa cca gct ctc aac aag att tct	2448						
Asp Met Ser Val Ala Thr Ser Glu Gln Pro Ala Leu Asn Lys Ile Ser							
		805		810		815	
ctg aaa agg aga aag agc act cta aga acc aca aat gca tat ttt tat	2496						
Leu Lys Arg Arg Lys Ser Thr Leu Arg Thr Thr Asn Ala Tyr Phe Tyr							
		820		825		830	
tgg gtg acc cgg gag caa gga tca ttt gat tgg ttc aaa ggc gtt atg	2544						
Trp Val Thr Arg Glu Gln Gly Ser Phe Asp Trp Phe Lys Gly Val Met							
		835		840		845	
aac gaa gtg gct gaa ctt gat caa agg ggg gtc atc gag atg cat aac	2592						
Asn Glu Val Ala Glu Leu Asp Gln Arg Gly Val Ile Glu Met His Asn							
		850		855		860	
tac ttg acg agt gtt tat gag gaa ggg gat gct cgt tca gct ctc att	2640						
Tyr Leu Thr Ser Val Tyr Glu Glu Gly Asp Ala Arg Ser Ala Leu Ile							
		865		870		875	
acc atg gtc cag gca ctt aac cat gct aag aat ggg gtt gat att gta	2688						
Thr Met Val Gln Ala Leu Asn His Ala Lys Asn Gly Val Asp Ile Val							
		885		890		895	
tca ggc acc agg gtg agg aca cat ttt gct agg cca aat tgg aag aaa	2736						
Ser Gly Thr Arg Val Arg Thr His Phe Ala Arg Pro Asn Trp Lys Lys							
		900		905		910	
gta ttt tcc aag acc tta acc aag cat gca aat gca aga ata ggg gtt	2784						
Val Phe Ser Lys Thr Leu Thr Lys His Ala Asn Ala Arg Ile Gly Val							
		915		920		925	
ttc tac tgt ggt gca ccc gta tta gca aaa gaa ctc agc aaa ctc tgc	2832						
Phe Tyr Cys Gly Ala Pro Val Leu Ala Lys Glu Leu Ser Lys Leu Cys							
		930		935		940	
aaa gag tat aat caa aag ggt gca aca aag ttc gag ttt cac aaa gaa	2880						
Lys Glu Tyr Asn Gln Lys Gly Ala Thr Lys Phe Glu Phe His Lys Glu							
		945		950		955	
cat ttt tag	2889						
His Phe							

&lt;210&gt; 6

&lt;211&gt; 962

&lt;212&gt; PRT

&lt;213&gt; Nicotiana tabacum

&lt;400&gt; 6

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Gln Glu Leu Lys Ala Glu Leu Arg Arg Phe Ser Trp Ser His Gly His	
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Val	Leu	Thr	Leu	Trp	Ile	Leu	Ile	Met	Ile	Gly	Leu	Phe	Leu	Trp	Lys
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Thr	Lys	Leu	Ser	His	Phe	Val	Pro	Phe	Asp	Asp	Asn	Ile	Asn	Phe	His
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Lys	Thr	Val	Ala	Ala	Ala	Ile	Val	Thr	Gly	Ile	Ile	Leu	His	Ala	Gly
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 Cys Pro Ala Val Ser Pro Phe Glu Trp His Pro Phe Ser Ile Thr Ser  
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 Ala Pro Gly Asp Asp Tyr Leu Ser Ile His Ile Arg Gln Leu Gly Asp  
 690 695 700  
 Trp Thr Gln Glu Leu Lys Arg Val Phe Ser Glu Ala Cys Glu Arg Pro  
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 Glu Ala Gly Lys Ser Gly Leu Leu Arg Ala Asp Glu Asn Thr Lys Lys  
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 Ser Leu Pro Lys Leu Leu Ile Asp Gly Pro Tyr Gly Ala Pro Ala Gln  
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 Asp Tyr Arg Lys Tyr Asp Val Leu Leu Val Gly Leu Gly Ile Gly  
 755 760 765  
 Ala Thr Pro Phe Ile Ser Ile Leu Lys Asp Leu Leu Val Asn Ile Val  
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 Tyr Leu Thr Ser Val Tyr Glu Glu Gly Asp Ala Arg Ser Ala Leu Ile  
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 His Phe

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<211> 3733

<212> DNA

<213> Solanum tuberosum

<220>

<221> CDS

<222> (92)..(2980)

<223> coding for NADPH oxidase

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 Met Arg Gly Leu Pro Gly His  
 1 5  
 gaa cgc cgg tgg acg tcg gat acg gta tct tcc ggc aag gat tta agt 160  
 Glu Arg Arg Trp Thr Ser Asp Thr Val Ser Ser Gly Lys Asp Leu Ser  
 10 15 20  
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 Gly Glu Ser Ser Pro Gly Thr Asp Ser Gly Asn Ile Ser Gly Phe Ala

25	30	35	
tcc gag gag ttt gtt gaa gtt ata ctt gat ctt cag gat gat gat acg			256
Ser Glu Glu Phe Val Glu Val Ile Leu Asp Leu Gln Asp Asp Asp Thr			
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att att cta cgg agc gtt gaa ccg gct act gta atc aac att gat gct			304
Ile Ile Leu Arg Ser Val Glu Pro Ala Thr Val Ile Asn Ile Asp Ala			
	60	65	70
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Ser Asp Pro Ala Thr Gly Val Gly Ile Gly Gly Val Ser Ile Glu Thr			
	75	80	85
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Pro Ala Ser Leu Thr Ser Thr Ser Gly Thr Arg Ser Pro Thr Met Arg			
	90	95	100
cgg agt aca tcg aat aaa tta cgt cag ttt tca cag gag ttg aaa gct			448
Arg Ser Thr Ser Asn Lys Leu Arg Gln Phe Ser Gln Glu Leu Lys Ala			
	105	110	115
gag gct gtc gcg aaa gcg aag cat ttc tcg caa gag ctt aaa gcg gag			496
Glu Ala Val Ala Lys Ala Lys His Phe Ser Gln Glu Leu Lys Ala Glu			
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Leu Arg Arg Phe Ser Trp Ser His Gly His Ala Ser Arg Thr Phe Ser			
	140	145	150
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Pro Ala Ser Phe Phe Gln Asn Ala Val Gly Thr Gly Asn Gly Val			
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	170	175	180
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Asp Arg Thr Arg Ser Ser Ala His Lys Ala Leu Arg Gly Leu Lys Phe			
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Ile Ser Asn Asn Lys Thr Asn Gly Trp Asn Glu Val Glu Asn Asn Phe			
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Ala Lys Leu Ala Lys Asp Gly Tyr Leu Tyr Arg Ser Asp Phe Ala Gln			
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tgc atc ggt atg aag gat tca aag gaa ttt gca ttg gaa ttg ttt gat			832
Cys Ile Gly Met Lys Asp Ser Lys Glu Phe Ala Leu Glu Leu Phe Asp			
	235	240	245
gct ttg agt aga aga aga ttg aag gtt gat aag att agc aaa gag			880
Ala Leu Ser Arg Arg Arg Arg Leu Lys Val Asp Lys Ile Ser Lys Glu			
	250	255	260
gaa ttg tat gag tat tgg tct caa atc acc gat cag agt ttc gat tct			928
Glu Leu Tyr Glu Tyr Trp Ser Gln Ile Thr Asp Gln Ser Phe Asp Ser			
	265	270	275
cgg ctt cag atc ttc ttc gac atg gtg gac aag aat gaa gat ggt cga			976
Arg Leu Gln Ile Phe Phe Asp Met Val Asp Lys Asn Glu Asp Gly Arg			
	280	285	290
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Ile Gly Glu Glu Glu Val Lys Glu Ile Ile Met Leu Ser Ala Ser Ala			
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Asn Lys Leu Ser Arg Leu Lys Glu Gln Ala Glu Glu Tyr Ala Ala Leu			
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Gln Leu Glu Thr Leu Leu Leu Gln Lys Asp Thr Tyr Leu Asn Tyr Ser			
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Leu Arg Lys Arg Ser Pro Ile Arg Arg Met Ser Thr Lys Leu Val Tyr	
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Ser Leu Gln Glu Asn Trp Lys Arg Ile Trp Val Leu Val Leu Trp Ile	
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Leu Ile Met Ile Gly Leu Phe Leu Trp Lys Phe Tyr Leu Tyr Lys Gln	
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Lys Ser Ala Phe Gln Val Met Gly Tyr Cys Leu Leu Thr Ala Lys Gly	
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Ala Ala Glu Thr Leu Lys Phe Asn Met Ala Leu Ile Leu Leu Pro Val	
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Cys Arg Asn Thr Ile Thr Phe Leu Arg Ser Thr Lys Leu Ser Cys Phe	
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Val Pro Phe Asp Asn Ile Asn Phe His Lys Thr Val Ala Ala Ala	
475 480 485	
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Ile Val Thr Gly Ile Ile Leu His Ala Gly Asn His Leu Val Cys Asp	
490 495 500	
ttc cca aag ctt ata cat gca aat aat acg aat tat cag aaa tat ttg	1648
Phe Pro Lys Leu Ile His Ala Asn Asn Thr Asn Tyr Gln Lys Tyr Leu	
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gtg aat gat ttt ggc cca agc cag cct cag tac ata gat ctt gtt aaa	1696
Val Asn Asp Phe Gly Pro Ser Gln Pro Gln Tyr Ile Asp Leu Val Lys	
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Gly Val Glu Gly Val Thr Gly Ile Ile Met Val Ile Leu Met Ala Ile	
540 545 550	
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Ala Phe Thr Leu Ala Thr Arg Trp Phe Arg Arg Ser Leu Ile Lys Phe	
555 560 565	
ccc aaa cct ttt gat aga ctc act ggt ttc aat gcg ttc tgg tac tcg	1840
Pro Lys Pro Phe Asp Arg Leu Thr Gly Phe Asn Ala Phe Trp Tyr Ser	
570 575 580	
cac cac ctt ctc atc att gtc tac atc gta ctg atc atc cat ggc aca	1888
His His Leu Leu Ile Ile Val Tyr Ile Val Leu Ile Ile His Gly Thr	
585 590 595	
ttc ctc tac ctt gtg cat aac tgg tac tcc aaa acg aca tgg atg tat	1936
Phe Leu Tyr Leu Val His Asn Trp Tyr Ser Lys Thr Thr Trp Met Tyr	
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Leu Ala Val Pro Val Leu Leu Tyr Ala Gly Glu Arg Thr Leu Arg Phe	
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635 640 645	
cct gga aat gtc ctt act ctg caa atg tct aag cct ccg caa ttt cga	2080
Pro Gly Asn Val Leu Thr Leu Gln Met Ser Lys Pro Pro Gln Phe Arg	
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Tyr Lys Ser Gly Gln Tyr Met Phe Val Gln Cys Pro Ala Val Ser Pro	
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Phe 680	Glu	Trp	His	Pro	Phe 685	Ser	Ile	Thr	Ser	Ala 690	Pro	Gly	Asp	Asp	Tyr 695			
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<210> 8

<211> 963

<212> PRT

<213> Solanum tuberosum

<400> 8

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 35          40          45
Asp Leu Gln Asp Asp Asp Thr Ile Ile Leu Arg Ser Val Glu Pro Ala
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Thr Val Ile Asn Ile Asp Ala Ser Asp Pro Ala Thr Gly Val Gly Ile
 65          70          75          80
Gly Gly Val Ser Ile Glu Thr Pro Ala Ser Leu Thr Ser Thr Ser Gly
 85          90          95
Thr Arg Ser Pro Thr Met Arg Arg Ser Thr Ser Asn Lys Leu Arg Gln
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Phe Ser Gln Glu Leu Lys Ala Glu Ala Val Ala Lys Ala Lys His Phe
115          120          125
Ser Gln Glu Leu Lys Ala Glu Leu Arg Arg Phe Ser Trp Ser His Gly
130          135          140
His Ala Ser Arg Thr Phe Ser Pro Ala Ser Phe Phe Gln Asn Ala Val
145          150          155          160
Val Gly Thr Gly Asn Gly Val Asp Ser Ala Leu Ala Ala Arg Ala Leu
165          170          175
Arg Arg Gln Arg Ala Gln Leu Asp Arg Thr Arg Ser Ser Ala His Lys
180          185          190
Ala Leu Arg Gly Leu Lys Phe Ile Ser Asn Asn Lys Thr Asn Gly Trp
195          200          205
Asn Glu Val Glu Asn Asn Phe Ala Lys Leu Ala Lys Asp Gly Tyr Leu
210          215          220
Tyr Arg Ser Asp Phe Ala Gln Cys Ile Gly Met Lys Asp Ser Lys Glu
225          230          235          240
Phe Ala Leu Glu Leu Phe Asp Ala Leu Ser Arg Arg Arg Arg Leu Lys
245          250          255
Val Asp Lys Ile Ser Lys Glu Glu Leu Tyr Glu Tyr Trp Ser Gln Ile
260          265          270
Thr Asp Gln Ser Phe Asp Ser Arg Leu Gln Ile Phe Phe Asp Met Val
275          280          285
Asp Lys Asn Glu Asp Gly Arg Ile Gly Glu Glu Glu Val Lys Glu Ile
290          295          300
Ile Met Leu Ser Ala Ser Ala Asn Lys Leu Ser Arg Leu Lys Glu Gln
305          310          315          320
Ala Glu Glu Tyr Ala Ala Leu Ile Met Glu Glu Leu Asp Pro Glu Arg
325          330          335
Leu Gly Tyr Ile Glu Leu Trp Gln Leu Glu Thr Leu Leu Leu Gln Lys
340          345          350
Asp Thr Tyr Leu Asn Tyr Ser Gln Ala Leu Ser Tyr Thr Ser Gln Ala
355          360          365
Leu Ser Gln Asn Leu Gln Gly Leu Arg Lys Arg Ser Pro Ile Arg Arg
370          375          380
Met Ser Thr Lys Leu Val Tyr Ser Leu Gln Glu Asn Trp Lys Arg Ile

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385					390					395					400
Trp	Val	Leu	Val	Leu	Trp	Ile	Leu	Ile	Met	Ile	Gly	Leu	Phe	Leu	Trp
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Lys	Phe	Tyr	Leu	Tyr	Lys	Gln	Lys	Ser	Ala	Phe	Gln	Val	Met	Gly	Tyr
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Cys	Leu	Leu	Thr	Ala	Lys	Gly	Ala	Ala	Glu	Thr	Leu	Lys	Phe	Asn	Met
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Ala	Leu	Ile	Leu	Leu	Pro	Val	Cys	Arg	Asn	Thr	Ile	Thr	Phe	Leu	Arg
	450					455				460					
Ser	Thr	Lys	Leu	Ser	Cys	Phe	Val	Pro	Phe	Asp	Asp	Asn	Ile	Asn	Phe
465					470					475					480
His	Lys	Thr	Val	Ala	Ala	Ala	Ile	Val	Thr	Gly	Ile	Ile	Leu	His	Ala
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Thr	Asn	Tyr	Gln	Lys	Tyr	Leu	Val	Asn	Asp	Phe	Gly	Pro	Ser	Gln	Pro
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Gln	Tyr	Ile	Asp	Leu	Val	Lys	Gly	Val	Glu	Gly	Val	Thr	Gly	Ile	Ile
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Met	Val	Ile	Leu	Met	Ala	Ile	Ala	Phe	Thr	Leu	Ala	Thr	Arg	Trp	Phe
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Arg	Arg	Ser	Leu	Ile	Lys	Phe	Pro	Lys	Pro	Phe	Asp	Arg	Leu	Thr	Gly
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Phe	Asn	Ala	Phe	Trp	Tyr	Ser	His	His	Leu	Leu	Ile	Ile	Val	Tyr	Ile
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Leu	Leu	Lys	Val	Ala	Ile	Tyr	Pro	Gly	Asn	Val	Leu	Thr	Leu	Gln	Met
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Gln	Cys	Pro	Ala	Val	Ser	Pro	Phe	Glu	Trp	His	Pro	Phe	Ser	Ile	Thr
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Ser	Ala	Pro	Gly	Asp	Asp	Tyr	Leu	Ser	Ile	His	Ile	Arg	Gln	Leu	Gly
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Asp	Trp	Thr	Gln	Glu	Leu	Lys	Arg	Val	Phe	Ser	Glu	Ala	Cys	Glu	Gln
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Pro	Glu	Ala	Gly	Lys	Ser	Gly	Leu	Leu	Arg	Ala	Asp	Glu	Asn	Thr	Lys
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Gln	Asp	Tyr	Arg	Lys	Tyr	Asp	Val	Leu	Leu	Leu	Val	Gly	Leu	Gly	Ile
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Gly	Ala	Thr	Pro	Phe	Ile	Ser	Ile	Leu	Lys	Asp	Leu	Leu	Lys	Asn	Ile
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Val	Thr	Met	Glu	Glu	Gln	Ala	Asp	Leu	Val	Ser	Asp	Phe	Ser	Gly	Asn
785					790					795					800
Ser	Asp	Met	Ser	Ala	Ala	Thr	Ser	Glu	Gln	Pro	Ala	Leu	Asn	Lys	Ile
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Ser	Pro	Lys	Lys	Arg	Lys	Ser	Thr	Leu	Lys	Thr	Thr	Asn	Ala	Tyr	Phe
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Tyr	Trp	Val	Thr	Arg	Glu	Gln	Gly	Ser	Phe	Asp	Trp	Phe	Lys	Gly	Val
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Met	Asn	Glu	Val	Ala	Glu	Leu	Asp	Gln	Arg	Gly	Val	Ile	Glu	Met	His
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Asn	Tyr	Leu	Thr	Ser	Val	Tyr	Glu	Glu	Gly	Asp	Ala	Arg	Ser	Ala	Leu
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Ile	Thr	Met	Val	Gln	Ala	Leu	Asn	His	Ala	Lys	Asn	Gly	Val	Asp	Ile
				885					890					895	
Val	Ser	Gly	Thr	Ser	Val	Arg	Thr	His	Phe	Ala	Arg	Pro	Asn	Trp	Arg
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Lys	Val	Phe	Ser	Lys	Thr	Leu	Thr	Lys	His	Ala	Asn	Ala	Arg	Ile	Gly
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Val	Phe	Tyr	Cys	Gly	Ala	Pro	Ile	Leu	Ala	Lys	Glu	Leu	Ser	Lys	Leu
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Cys	Lys	Glu	Phe	Asn	Gln	Lys	Gly	Thr	Thr	Lys	Phe	Glu	Phe	His	Lys
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Glu	His	Phe													

&lt;210&gt; 9

&lt;211&gt; 3316

&lt;212&gt; DNA

&lt;213&gt; Lycopersicon esculentum

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (146)..(3112)

&lt;223&gt; coding for NADPH oxidase

&lt;400&gt; 9

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		Met Arg Gly Leu	Pro Gly His Glu Arg			
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cgg tgg acg tcg gat acg gtg tct tcc ggg aag gat tta agt ggt gag						220
Arg Trp Thr Ser Asp Thr Val Ser Ser Gly Lys Asp Leu Ser Gly Glu						
10	15	20	25			
tca tcg ccg gga act gat tcc ggg aat att tcc ggt ttt gct tcg gag						268
Ser Ser Pro Gly Thr Asp Ser Gly Asn Ile Ser Gly Phe Ala Ser Glu						
	30	35	40			
gag ttt gtt gaa gtt ata ctt gat ctt cag gat gat gat acg att att						316
Glu Phe Val Glu Val Ile Leu Asp Leu Gln Asp Asp Asp Thr Ile Ile						
	45	50	55			
tta cgg agc gtt gaa ccg gct act gta atc aac att gat ggt tct gat						364
Leu Arg Ser Val Glu Pro Ala Thr Val Ile Asn Ile Asp Gly Ser Asp						
	60	65	70			
cct gct tcc gga gtc ggt att ggt gga gca tcg att gaa act ccg gcg						412
Pro Ala Ser Gly Val Gly Ile Gly Gly Ala Ser Ile Glu Thr Pro Ala						
	75	80	85			
tcg gtg acg tcg acg tcg gaa act cga tcg ccg atg atg cgt cgg agt						460
Ser Val Thr Ser Thr Ser Glu Thr Arg Ser Pro Met Met Arg Arg Ser						
	90	95	100			105
aca tct aat aag ttt cgt cag ttt tca cag gag ttg aaa gct gag gct						508
Thr Ser Asn Lys Phe Arg Gln Phe Ser Gln Glu Leu Lys Ala Glu Ala						
	110	115	120			
gtt gcg aaa gcg aag cat ttc tcg caa gag ctt aaa gcg gag cta agg						556
Val Ala Lys Ala Lys His Phe Ser Gln Glu Leu Lys Ala Glu Leu Arg						
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aga ttc tca tgg agc cat gga cat gcg tct cgt gct ttt tcg ccg gcg						604
Arg Phe Ser Trp Ser His Gly His Ala Ser Arg Ala Phe Ser Pro Ala						
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tcg ttt ttc caa aac gct gtc gtc gga aca ggc aac ggt gta gac tcg						652
Ser Phe Phe Gln Asn Ala Val Val Gly Thr Gly Asn Gly Val Asp Ser						
	155	160	165			
gct tta gcg gct cga gca tta cgt cgg cag cgt gct cag ctc gac cgg						700
Ala Leu Ala Ala Arg Ala Leu Arg Arg Gln Arg Ala Gln Leu Asp Arg						

170					175					180					185	
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Thr	Arg	Ser	Ser	Ala	His	Lys	Ala	Leu	Arg	Gly	Leu	Lys	Phe	Ile	Ser	
				190					195					200		
aat	aac	aaa	act	aac	gga	tgg	aat	gaa	gtt	gaa	aac	aat	ttc	gct	aag	796
Asn	Asn	Lys	Thr	Asn	Gly	Trp	Asn	Glu	Val	Glu	Asn	Asn	Phe	Ala	Lys	
			205					210					215			
ctc	gct	aaa	gac	ggg	tac	ctt	tat	cgt	tcc	gat	ttc	gca	caa	tgc	atc	844
Leu	Ala	Lys	Asp	Gly	Tyr	Leu	Tyr	Arg	Ser	Asp	Phe	Ala	Gln	Cys	Ile	
		220					225					230				
ggg	cag	tac	tca	cgc	cgg	cga	tca	cta	cag	ttt	aat	tat	aga	tta	att	892
Gly	Gln	Tyr	Ser	Arg	Arg	Arg	Ser	Leu	Gln	Phe	Asn	Tyr	Arg	Leu	Ile	
	235				240						245					
aca	tta	att	ttg	att	aat	tat	ttg	gtt	aaa	ggg	atg	aag	gat	tca	aag	940
Thr	Leu	Ile	Leu	Ile	Asn	Tyr	Leu	Val	Lys	Gly	Met	Lys	Asp	Ser	Lys	
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Glu	Phe	Ala	Leu	Glu	Leu	Phe	Asp	Ala	Leu	Ser	Arg	Arg	Arg	Arg	Leu	
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aag	gtt	gat	aag	att	agc	caa	gag	gaa	ttg	tat	gag	tat	tgg	tct	caa	1036
Lys	Val	Asp	Lys	Ile	Ser	Gln	Glu	Glu	Leu	Tyr	Glu	Tyr	Trp	Ser	Gln	
			285					290					295			
atc	acc	gat	cag	agt	ttc	gat	tct	cgg	ctt	cag	atc	ttc	ttc	gac	atg	1084
Ile	Thr	Asp	Gln	Ser	Phe	Asp	Ser	Arg	Leu	Gln	Ile	Phe	Phe	Asp	Met	
		300				305						310				
gtg	gac	aag	aat	gaa	gat	ggg	cga	att	ggg	gaa	gaa	gaa	gta	aaa	gag	1132
Val	Asp	Lys	Asn	Glu	Asp	Gly	Arg	Ile	Gly	Glu	Glu	Glu	Val	Lys	Glu	
	315				320					325						
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Ile	Ile	Met	Leu	Ser	Ala	Ser	Ala	Asn	Lys	Leu	Ser	Arg	Leu	Lys	Glu	
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Gln	Ala	Glu	Glu	Tyr	Ala	Ala	Leu	Ile	Met	Glu	Glu	Leu	Asp	Pro	Glu	
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Arg	Leu	Gly	Tyr	Ile	Glu	Leu	Trp	Gln	Leu	Glu	Thr	Leu	Leu	Leu	Gln	
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Lys	Asp	Thr	Tyr	Leu	Asn	Tyr	Ser	Gln	Ala	Leu	Ser	Tyr	Thr	Ser	Gln	
		380				385						390				
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Ala	Leu	Ser	Gln	Asn	Leu	Gln	Gly	Leu	Arg	Lys	Arg	Ser	Pro	Ile	Arg	
	395				400					405						
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Arg	Met	Ser	Thr	Lys	Leu	Val	Tyr	Ser	Leu	Gln	Glu	Asn	Trp	Lys	Arg	
410				415						420				425		
att	tgg	gtt	ctg	gtc	ttg	tgg	att	ttg	ata	atg	att	gga	ctt	ttt	ctt	1468
Ile	Trp	Val	Leu	Val	Leu	Trp	Ile	Leu	Ile	Met	Ile	Gly	Leu	Phe	Leu	
			430					435					440			
tgg	aag	ttc	tat	cag	tac	aaa	cag	aaa	agt	gca	ttt	caa	gtc	atg	ggg	1516
Trp	Lys	Phe	Tyr	Gln	Tyr	Lys	Gln	Lys	Ser	Ala	Phe	Gln	Val	Met	Gly	
		445					450					455				
tat	tgc	ctt	cta	aca	gct	aag	ggg	gct	gct	gag	act	ctc	aag	ttc	aac	1564
Tyr	Cys	Leu	Leu	Thr	Ala	Lys	Gly	Ala	Ala	Glu	Thr	Leu	Lys	Phe	Asn	
		460			465							470				
atg	gct	tta	ata	ttg	ttg	cca	gta	tgc	agg	aac	acc	att	aca	ttc	ctc	1612
Met	Ala	Leu	Ile	Leu	Leu	Pro	Val	Cys	Arg	Asn	Thr	Ile	Thr	Phe	Leu	
	475				480					485						
agg	tct	act	aaa	ttg	agc	tgt	ttt	gta	ccc	ttt	gat	gac	aac	ata	aac	1660
Arg	Ser	Thr	Lys	Leu	Ser	Cys	Phe	Val	Pro	Phe	Asp	Asp	Asn	Ile	Asn	
490				495						500				505		

ttt	cac	aag	act	gtt	gct	gca	gcc	att	gtc	act	ggt	atc	ata	ctc	cat	1708
Phe	His	Lys	Thr	Val	Ala	Ala	Ala	Ile	Val	Thr	Gly	Ile	Ile	Leu	His	
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gcc	ggt	aat	cac	ctt	gta	tgt	gat	ttc	cca	aag	ctt	ata	cat	gca	aat	1756
Ala	Gly	Asn	His	Leu	Val	Cys	Asp	Phe	Pro	Lys	Leu	Ile	His	Ala	Asn	
			525					530						535		
agt	acg	aat	tat	cag	aaa	tat	ttg	gtg	aat	gat	ttt	ggc	cca	agc	cag	1804
Ser	Thr	Asn	Tyr	Gln	Lys	Tyr	Leu	Val	Asn	Asp	Phe	Gly	Pro	Ser	Gln	
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Pro	Gln	Tyr	Ile	Asp	Leu	Val	Lys	Gly	Val	Glu	Gly	Val	Thr	Gly	Ile	
	555					560					565					
gtt	atg	gta	atc	ctc	atg	gcc	att	gct	ttc	act	ctt	gca	acg	cga	tgg	1900
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Phe	Arg	Arg	Ser	Leu	Ile	Lys	Leu	Pro	Lys	Pro	Phe	Asp	Arg	Leu	Thr	
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ggt	ttc	aat	gcg	ttc	tgg	tac	tcg	cac	cac	ctt	ctc	atc	att	gtc	tac	1996
Gly	Phe	Asn	Ala	Phe	Trp	Tyr	Ser	His	His	Leu	Leu	Ile	Ile	Val	Tyr	
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Ile	Val	Leu	Ile	Ile	His	Gly	Thr	Phe	Leu	Tyr	Leu	Val	His	Asn	Trp	
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Tyr	Ser	Lys	Thr	Thr	Trp	Met	Tyr	Ile	Ala	Val	Pro	Val	Leu	Leu	Tyr	
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Ala	Gly	Glu	Arg	Thr	Leu	Arg	Phe	Phe	Arg	Ser	Gly	Leu	Tyr	Ser	Val	
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Arg	Leu	Leu	Lys	Val	Ala	Ile	Tyr	Pro	Gly	Asn	Val	Leu	Thr	Leu	Gln	
			670						675					680		
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Met	Ser	Lys	Pro	Pro	Gln	Phe	Arg	Tyr	Lys	Ser	Gly	Gln	Tyr	Met	Phe	
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Val	Gln	Cys	Pro	Ala	Val	Ser	Pro	Phe	Glu	Trp	His	Pro	Phe	Ser	Ile	
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Thr	Ser	Ala	Pro	Gly	Asp	Asp	Tyr	Leu	Ser	Ile	His	Ile	Arg	Gln	Leu	
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Gly	Asp	Trp	Thr	Gln	Glu	Leu	Lys	Arg	Val	Phe	Ser	Glu	Ala	Cys	Glu	
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Gln	Pro	Glu	Ala	Gly	Lys	Ser	Gly	Leu	Leu	Arg	Ala	Asp	Glu	Asn	Thr	
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Lys	Thr	Ser	Leu	Pro	Lys	Leu	Leu	Ile	Asp	Gly	Pro	Tyr	Gly	Ala	Pro	
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Ala	Gln	Asp	Tyr	Arg	Lys	Tyr	Asp	Val	Leu	Leu	Leu	Val	Gly	Leu	Gly	
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Ile	Gly	Ala	Thr	Pro	Phe	Ile	Ser	Ile	Leu	Lys	Asp	Leu	Leu	Lys	Asn	
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Ile	Val	Ala	Met	Glu	Glu	Gln	Ala	Asp	Leu	Val	Ser	Asp	Phe	Ser	Gly	
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Ile Ser Pro Lys Lys Arg Lys Ser Thr Leu Lys Thr Thr Asn Ala Tyr
      845      850      855
ttt tat tgg gtg acc cgg gag caa gga tca ttt gat tgg ttc aaa ggt 2764
Phe Tyr Trp Val Thr Arg Glu Gln Gly Ser Phe Asp Trp Phe Lys Gly
      860      865      870
gtt atg aat gaa gtg gct gaa ctt gat caa agg ggt gtc atc gag atg 2812
Val Met Asn Glu Val Ala Glu Leu Asp Gln Arg Gly Val Ile Glu Met
      875      880      885
cat aac tac ttg acg agt gtt tat gag gaa ggg gat gca cgt tca gct 2860
His Asn Tyr Leu Thr Ser Val Tyr Glu Glu Gly Asp Ala Arg Ser Ala
      890      895      900
ctc att acc atg gtc cag gca ctt aac cat gct aag aat ggg gtt gat 2908
Leu Ile Thr Met Val Gln Ala Leu Asn His Ala Lys Asn Gly Val Asp
      910      915      920
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Ile Val Ser Gly Thr Ser Val Arg Thr His Phe Ala Arg Pro Asn Trp
      925      930      935
agg aaa gta ttt tcc aag acc tta acc aag cat gca aat gca aga ata 3004
Arg Lys Val Phe Ser Lys Thr Leu Thr Lys His Ala Asn Ala Arg Ile
      940      945      950
gga gtt ttc tac tgt ggt gca ccc ata tta gct aaa gaa ctc agc caa 3052
Gly Val Phe Tyr Cys Gly Ala Pro Ile Leu Ala Lys Glu Leu Ser Gln
      955      960      965
ctc tgc aaa gag ttt aac caa aag ggc aca aca aag ttc gag ttt cac 3100
Leu Cys Lys Glu Phe Asn Gln Lys Gly Thr Thr Lys Phe Glu Phe His
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Lys Glu His Phe
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<210> 10

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Gly Asn Ile Ser Gly Phe Ala Ser Glu Glu Phe Val Glu Val Ile Leu
      35      40      45
Asp Leu Gln Asp Asp Asp Thr Ile Ile Leu Arg Ser Val Glu Pro Ala
      50      55      60
Thr Val Ile Asn Ile Asp Gly Ser Asp Pro Ala Ser Gly Val Gly Ile
      65      70      75      80
Gly Gly Ala Ser Ile Glu Thr Pro Ala Ser Val Thr Ser Thr Ser Glu
      85      90      95
Thr Arg Ser Pro Met Met Arg Arg Ser Thr Ser Asn Lys Phe Arg Gln
      100      105      110
Phe Ser Gln Glu Leu Lys Ala Glu Ala Val Ala Lys Ala Lys His Phe
      115      120      125
Ser Gln Glu Leu Lys Ala Glu Leu Arg Arg Phe Ser Trp Ser His Gly
      130      135      140
His Ala Ser Arg Ala Phe Ser Pro Ala Ser Phe Phe Gln Asn Ala Val
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Val	Gly	Thr	Gly	Asn	Gly	Val	Asp	Ser	Ala	Leu	Ala	Ala	Arg	Ala	Leu
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Ser	Thr	Leu	Lys	Thr	Thr	Asn	Ala	Tyr	Phe	Tyr	Trp	Val	Thr	Arg	Glu
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Ser	Phe	Asp	Ser	Val	Ser	Ala	Gly	Lys	Thr	Ala	Val	Gly	Ser	Ala	Ser	
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Phe	Thr	Leu	Ala	Thr	Arg	Trp	Phe	Arg	Arg	Asn	Leu	Val	Lys	Leu	Pro	
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720                725                730
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His Asn Tyr Leu Thr Ser Val Tyr Glu Glu Gly Asp Ala Arg Ser Ala
845                850                855                860
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910                915                920
cta tgc aac aca ttc aat caa aaa ggt tca acc aag ttt gaa ttt cac 2834
Leu Cys Asn Thr Phe Asn Gln Lys Gly Ser Thr Lys Phe Glu Phe His
925                930                935                940
aag gag cat ttc taaaagacaa gaaggaagaa gccaaaagcc ctctagattc 2886
Lys Glu His Phe
ttaaataatct caaatttagc cacttatagt ataaaggcaa tctcttcact atttaattca 2946
aagtgattaa acgttaacac actgtcaaaa gtgagtgtgt taacgttttag ctccacacgt 3006
tctaggttta tatacaccga ggcatacgtg taaatatacg agacagaaga aattcaaggg 3066
ggtttgatag aagc 3080

```

&lt;210&gt; 12

&lt;211&gt; 944

&lt;212&gt; PRT

&lt;213&gt; Arabidopsis thaliana

&lt;400&gt; 12

Met	Lys	Pro	Phe	Ser	Lys	Asn	Asp	Arg	Arg	Arg	Trp	Ser	Phe	Asp	Ser	1	5	10	15
Val	Ser	Ala	Gly	Lys	Thr	Ala	Val	Gly	Ser	Ala	Ser	Thr	Ser	Pro	Gly	20	25	30	
Thr	Glu	Tyr	Ser	Ile	Asn	Gly	Asp	Gln	Glu	Phe	Val	Glu	Val	Thr	Ile	35	40	45	
Asp	Leu	Gln	Asp	Asp	Asp	Thr	Ile	Val	Leu	Arg	Ser	Val	Glu	Pro	Ala	50	55	60	
Thr	Ala	Ile	Asn	Val	Ile	Gly	Asp	Ile	Ser	Asp	Asp	Asn	Thr	Gly	Ile	65	70	75	80
Met	Thr	Pro	Val	Ser	Ile	Ser	Arg	Ser	Pro	Thr	Met	Lys	Arg	Thr	Ser	85	90		95
Ser	Asn	Arg	Phe	Arg	Gln	Phe	Ser	Gln	Glu	Leu	Lys	Ala	Glu	Ala	Val	100	105	110	
Ala	Lys	Ala	Lys	Gln	Leu	Ser	Gln	Glu	Leu	Lys	Arg	Phe	Ser	Trp	Ser	115	120	125	
Arg	Ser	Phe	Ser	Gly	Asn	Leu	Thr	Thr	Thr	Ser	Thr	Ala	Ala	Asn	Gln	130	135	140	
Ser	Gly	Gly	Ala	Gly	Gly	Gly	Leu	Val	Asn	Ser	Ala	Leu	Glu	Ala	Arg	145	150	155	160
Ala	Leu	Arg	Lys	Gln	Arg	Ala	Gln	Leu	Asp	Arg	Thr	Arg	Ser	Ser	Ala	165	170		175
Gln	Arg	Ala	Leu	Arg	Gly	Leu	Arg	Phe	Ile	Ser	Asn	Lys	Gln	Lys	Asn	180	185	190	
Val	Asp	Gly	Trp	Asn	Asp	Val	Gln	Ser	Asn	Phe	Glu	Lys	Phe	Glu	Lys	195	200	205	
Asn	Gly	Tyr	Ile	Tyr	Arg	Ser	Asp	Phe	Ala	Gln	Cys	Ile	Gly	Met	Lys	210	215	220	
Asp	Ser	Lys	Glu	Phe	Ala	Leu	Glu	Leu	Phe	Asp	Ala	Leu	Ser	Arg	Arg	225	230	235	240
Arg	Arg	Leu	Lys	Val	Glu	Lys	Ile	Asn	His	Asp	Glu	Leu	Tyr	Glu	Tyr	245	250		255
Trp	Ser	Gln	Ile	Asn	Asp	Glu	Ser	Phe	Asp	Ser	Arg	Leu	Gln	Ile	Phe	260	265	270	
Phe	Asp	Ile	Val	Asp	Lys	Asn	Glu	Asp	Gly	Arg	Ile	Thr	Glu	Glu	Glu	275	280	285	
Val	Lys	Glu	Ile	Ile	Met	Leu	Ser	Ala	Ser	Ala	Asn	Lys	Leu	Ser	Arg	290	295	300	
Leu	Lys	Glu	Gln	Ala	Glu	Glu	Tyr	Ala	Ala	Leu	Ile	Met	Glu	Glu	Leu	305	310	315	320
Asp	Pro	Glu	Arg	Leu	Gly	Tyr	Ile	Glu	Leu	Trp	Gln	Leu	Glu	Thr	Leu	325	330		335
Leu	Leu	Gln	Lys	Asp	Thr	Tyr	Leu	Asn	Tyr	Ser	Gln	Ala	Leu	Ser	Tyr	340	345	350	
Thr	Ser	Gln	Ala	Leu	Ser	Gln	Asn	Leu	Gln	Gly	Leu	Arg	Gly	Lys	Ser	355	360	365	
Arg	Ile	His	Arg	Met	Ser	Ser	Asp	Phe	Val	Tyr	Ile	Met	Gln	Glu	Asn	370	375	380	
Trp	Lys	Arg	Ile	Trp	Val	Leu	Ser	Leu	Trp	Ile	Met	Ile	Met	Ile	Gly	385	390	395	400
Leu	Phe	Leu	Trp	Lys	Phe	Phe	Gln	Tyr	Lys	Gln	Lys	Asp	Ala	Phe	His	405	410		415
Val	Met	Gly	Tyr	Cys	Leu	Leu	Thr	Ala	Lys	Gly	Ala	Ala	Glu	Thr	Leu	420	425	430	
Lys	Phe	Asn	Met	Ala	Leu	Ile	Leu	Phe	Pro	Val	Cys	Arg	Asn	Thr	Ile	435	440	445	
Thr	Trp	Leu	Arg	Ser	Thr	Arg	Leu	Ser	Tyr	Phe	Val	Pro	Phe	Asp	Asp	450	455	460	
Asn	Ile	Asn	Phe	His	Lys	Thr	Ile	Ala	Gly	Ala	Ile	Val	Val	Ala	Val	465	470	475	480

Ile	Leu	His	Ile	Gly	Asp	His	Leu	Ala	Cys	Asp	Phe	Pro	Arg	Ile	Val
				485					490					495	
Arg	Ala	Thr	Glu	Tyr	Asp	Tyr	Asn	Arg	Tyr	Leu	Phe	His	Tyr	Phe	Gln
			500					505					510		
Thr	Lys	Gln	Pro	Thr	Tyr	Phe	Asp	Leu	Val	Lys	Gly	Pro	Glu	Gly	Ile
		515					520					525			
Thr	Gly	Ile	Leu	Met	Val	Ile	Leu	Met	Ile	Ile	Ser	Phe	Thr	Leu	Ala
	530					535					540				
Thr	Arg	Trp	Phe	Arg	Arg	Asn	Leu	Val	Lys	Leu	Pro	Lys	Pro	Phe	Asp
545					550					555					560
Arg	Leu	Thr	Gly	Phe	Asn	Ala	Phe	Trp	Tyr	Ser	His	His	Leu	Phe	Val
			565						570					575	
Ile	Val	Tyr	Ile	Leu	Leu	Ile	Leu	His	Gly	Ile	Phe	Leu	Tyr	Phe	Ala
			580					585					590		
Lys	Pro	Trp	Tyr	Val	Arg	Thr	Thr	Trp	Met	Tyr	Leu	Ala	Val	Pro	Val
		595					600					605			
Leu	Leu	Tyr	Gly	Gly	Glu	Arg	Thr	Leu	Arg	Tyr	Phe	Arg	Ser	Gly	Ser
	610					615					620				
Tyr	Ser	Val	Arg	Leu	Leu	Lys	Val	Ala	Ile	Tyr	Pro	Gly	Asn	Val	Leu
625					630					635					640
Thr	Leu	Gln	Met	Ser	Lys	Pro	Thr	Gln	Phe	Arg	Tyr	Lys	Ser	Gly	Gln
			645						650					655	
Tyr	Met	Phe	Val	Gln	Cys	Pro	Ala	Val	Ser	Pro	Phe	Glu	Trp	His	Pro
			660					665					670		
Phe	Ser	Ile	Thr	Ser	Ala	Pro	Glu	Asp	Asp	Tyr	Ile	Ser	Ile	His	Ile
		675					680					685			
Arg	Gln	Leu	Gly	Asp	Trp	Thr	Gln	Glu	Leu	Lys	Arg	Val	Phe	Ser	Glu
	690					695					700				
Val	Cys	Glu	Pro	Pro	Val	Gly	Gly	Lys	Ser	Gly	Leu	Leu	Arg	Ala	Asp
705					710					715					720
Glu	Thr	Thr	Lys	Lys	Ser	Leu	Pro	Lys	Leu	Leu	Ile	Asp	Gly	Pro	Tyr
			725						730					735	
Gly	Ala	Pro	Ala	Gln	Asp	Tyr	Arg	Lys	Tyr	Asp	Val	Leu	Leu	Leu	Val
			740					745					750		
Gly	Leu	Gly	Ile	Gly	Ala	Thr	Pro	Phe	Ile	Ser	Ile	Leu	Lys	Asp	Leu
		755					760					765			
Leu	Asn	Asn	Ile	Val	Lys	Met	Glu	Glu	His	Ala	Asp	Ser	Ile	Ser	Asp
	770					775					780				
Phe	Ser	Arg	Ser	Ser	Glu	Tyr	Ser	Thr	Gly	Ser	Asn	Gly	Asp	Thr	Pro
785					790					795					800
Arg	Arg	Lys	Arg	Ile	Leu	Lys	Thr	Thr	Asn	Ala	Tyr	Phe	Tyr	Trp	Val
			805						810					815	
Thr	Arg	Glu	Gln	Gly	Ser	Phe	Asp	Trp	Phe	Lys	Gly	Val	Met	Asn	Glu
		820						825					830		
Val	Ala	Glu	Leu	Asp	Gln	Arg	Gly	Val	Ile	Glu	Met	His	Asn	Tyr	Leu
		835					840					845			
Thr	Ser	Val	Tyr	Glu	Glu	Gly	Asp	Ala	Arg	Ser	Ala	Leu	Ile	Thr	Met
	850					855					860				
Val	Gln	Ala	Leu	Asn	His	Ala	Lys	Asn	Gly	Val	Asp	Ile	Val	Ser	Gly
865					870					875					880
Thr	Arg	Val	Arg	Thr	His	Phe	Ala	Arg	Pro	Asn	Trp	Lys	Lys	Val	Leu
			885						890					895	
Thr	Lys	Leu	Ser	Ser	Lys	His	Cys	Asn	Ala	Arg	Thr	Gly	Val	Phe	Tyr
		900						905					910		
Cys	Gly	Val	Pro	Val	Leu	Gly	Lys	Glu	Leu	Ser	Lys	Leu	Cys	Asn	Thr
		915					920					925			
Phe	Asn	Gln	Lys	Gly	Ser	Thr	Lys	Phe	Glu	Phe	His	Lys	Glu	His	Phe
	930					935					940				

&lt;210&gt; 13

&lt;211&gt; 3035

&lt;212&gt; DNA

&lt;213&gt; Arabidopsis thaliana

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (132)..(2894)

&lt;223&gt; coding for NADPH oxidase

&lt;400&gt; 13

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tcaaacacct tttgagagcg gttatTTTTT ctctatcaac taatacagta accttacggg 60
tgTTTTatttg tatagatctc tgtggttttc ttggccaact ctagtgagat ctttttcggt 120
tctcgaattc g atg aaa atg aga cga ggc aat tca agt aac gac cat gaa 170
          Met Lys Met Arg Arg Gly Asn Ser Ser Asn Asp His Glu
              1             5             10
ctt ggg att cta cga gga gct aac tcg gac acc aac tcg gac acg gag 218
Leu Gly Ile Leu Arg Gly Ala Asn Ser Asp Thr Asn Ser Asp Thr Glu
      15             20             25
agc atc gct agc gac cgt ggt gcc ttt agc ggt ccg ctt ggc cgg cct 266
Ser Ile Ala Ser Asp Arg Gly Ala Phe Ser Gly Pro Leu Gly Arg Pro
      30             35             40             45
aaa cgt gcg tcc aag aaa aac gca aga ttc gcc gac gat ctt ccc aag 314
Lys Arg Ala Ser Lys Lys Asn Ala Arg Phe Ala Asp Asp Leu Pro Lys
              50             55             60
aga agc aat agt gtt gct ggc ggc cgt ggt gat gac gat gag tac gtg 362
Arg Ser Asn Ser Val Ala Gly Gly Arg Gly Asp Asp Asp Glu Tyr Val
              65             70             75
gag atc acg cta gac atc agg gac gac tcg gtg gcc gtc cat agt gtc 410
Glu Ile Thr Leu Asp Ile Arg Asp Asp Ser Val Ala Val His Ser Val
              80             85             90
caa caa gca gct gga ggt gga ggc cac ctg gag gac ccg gag cta gcc 458
Gln Gln Ala Ala Gly Gly Gly Gly His Leu Glu Asp Pro Glu Leu Ala
      95             100             105
ctt ctt acg aag aag act ctc gag agc agc ctc aac aac acc acc tcc 506
Leu Leu Thr Lys Lys Thr Leu Glu Ser Ser Leu Asn Asn Thr Thr Ser
     110             115             120             125
tta tct ttc ttc cga agc acc tcc tca cgc atc aag aac gcc tcc cgc 554
Leu Ser Phe Phe Arg Ser Thr Ser Ser Arg Ile Lys Asn Ala Ser Arg
              130             135             140
gag ctc cgc cgc gtg ttc tct aga cgt ccc tcc ccg gcc gtg cgg cgg 602
Glu Leu Arg Arg Val Phe Ser Arg Arg Pro Ser Pro Ala Val Arg Arg
              145             150             155
ttt gac cgc acg agc tcc gcg gcc atc cac gca ctc aaa ggt ctc aag 650
Phe Asp Arg Thr Ser Ser Ala Ala Ile His Ala Leu Lys Gly Leu Lys
      160             165             170
ttc att gcc acc aag acg gcc gca tgg ccg gcc gtc gac caa cgt ttc 698
Phe Ile Ala Thr Lys Thr Ala Ala Trp Pro Ala Val Asp Gln Arg Phe
      175             180             185
gat aaa ctc tcc gct gat tcc aac ggc ctc tta ctc tct gcc aag ttt 746
Asp Lys Leu Ser Ala Asp Ser Asn Gly Leu Leu Leu Ser Ala Lys Phe
     190             195             200             205
tgg gaa tgc tta gga atg aat aag gaa tct aaa gac ttc gct gac cag 794
Trp Glu Cys Leu Gly Met Asn Lys Glu Ser Lys Asp Phe Ala Asp Gln
              210             215             220
ctc ttt aga gca tta gct cgc cgg aat aac gtc tcc ggc gat gca atc 842
Leu Phe Arg Ala Leu Ala Arg Arg Asn Asn Val Ser Gly Asp Ala Ile
      225             230             235
aca aag gaa cag ctt agg ata ttc tgg gaa cag atc tca gac gaa agc 890
Thr Lys Glu Gln Leu Arg Ile Phe Trp Glu Gln Ile Ser Asp Glu Ser
      240             245             250
ttt gat gcc aaa ctc caa gtc ttt ttt gac atg gtg gac aaa gat gaa 938
Phe Asp Ala Lys Leu Gln Val Phe Phe Asp Met Val Asp Lys Asp Glu

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255	gat	ggg	cga	gta	aca	gaa	gaa	gag	gtg	gct	gag	att	att	agt	ctt	agt	986
270	Asp	Gly	Arg	Val	Thr	Glu	Glu	Glu	Val	Ala	Glu	Ile	Ile	Ser	Leu	Ser	
						275					280					285	
	gct	tct	gca	aac	aag	ctc	tca	aat	att	caa	aag	caa	gcc	aaa	gaa	tat	1034
	Ala	Ser	Ala	Asn	Lys	Leu	Ser	Asn	Ile	Gln	Lys	Gln	Ala	Lys	Glu	Tyr	
					290					295					300		
	gcg	gca	ctg	ata	atg	gaa	gag	ttg	gac	cca	gac	aat	gct	ggg	ttt	att	1082
	Ala	Ala	Leu	Ile	Met	Glu	Glu	Leu	Asp	Pro	Asp	Asn	Ala	Gly	Phe	Ile	
					305				310					315			
	atg	atc	gaa	aac	ttg	gaa	atg	ttg	cta	tta	caa	gca	ccg	aac	cag	tcg	1130
	Met	Ile	Glu	Asn	Leu	Glu	Met	Leu	Leu	Gln	Ala	Pro	Asn	Gln	Ser		
					320			325				330					
	gtg	cgg	atg	gga	gac	agc	agg	ata	ctt	agt	cag	atg	tta	agt	cag	aag	1178
	Val	Arg	Met	Gly	Asp	Ser	Arg	Ile	Leu	Ser	Gln	Met	Leu	Ser	Gln	Lys	
					335			340				345					
	ctt	aga	ccg	gca	aaa	gag	agc	aac	cct	tta	ttg	aga	tggt	tcg	gag	aaa	1226
	Leu	Arg	Pro	Ala	Lys	Glu	Ser	Asn	Pro	Leu	Leu	Arg	Trp	Ser	Glu	Lys	
	350				355					360					365		
	atc	aaa	tat	ttc	ata	ctt	gat	aat	tgg	cag	aga	tta	tgg	atc	atg	atg	1274
	Ile	Lys	Tyr	Phe	Ile	Leu	Asp	Asn	Trp	Gln	Arg	Leu	Trp	Ile	Met	Met	
					370				375					380			
	tta	tgg	ctt	ggc	atc	tgt	ggg	ggc	ctc	ttt	act	tat	aaa	ttc	att	cag	1322
	Leu	Trp	Leu	Gly	Ile	Cys	Gly	Gly	Leu	Phe	Thr	Tyr	Lys	Phe	Ile	Gln	
					385				390					395			
	tac	aag	aac	aaa	gct	gcc	tat	ggg	gtg	atg	ggg	tat	tgt	gtt	tgt	gtc	1370
	Tyr	Lys	Asn	Lys	Ala	Ala	Tyr	Gly	Val	Met	Gly	Tyr	Cys	Val	Cys	Val	
					400			405				410					
	gcc	aaa	gga	ggc	gcc	gag	act	ctc	aaa	ttc	aac	atg	gct	ctc	ata	ttg	1418
	Ala	Lys	Gly	Gly	Ala	Glu	Thr	Leu	Lys	Phe	Asn	Met	Ala	Leu	Ile	Leu	
	415				420					425							
	ttg	cct	gtt	tgt	cga	aac	acc	atc	act	tgg	ctt	agg	aac	aag	acc	aag	1466
	Leu	Pro	Val	Cys	Arg	Asn	Thr	Ile	Thr	Trp	Leu	Arg	Asn	Lys	Thr	Lys	
	430				435					440					445		
	ctt	ggg	act	gtc	gtt	cct	ttt	gat	gat	agt	ctt	aac	ttc	cac	aag	gtt	1514
	Leu	Gly	Thr	Val	Val	Pro	Phe	Asp	Asp	Ser	Leu	Asn	Phe	His	Lys	Val	
					450					455					460		
	att	gca	agc	ggg	ata	gtc	gtc	ggg	gtt	ttg	ctc	cat	gcg	ggg	gcc	cat	1562
	Ile	Ala	Ser	Gly	Ile	Val	Val	Gly	Val	Leu	Leu	His	Ala	Gly	Ala	His	
					465			470						475			
	tta	acg	tgt	gat	ttt	cca	cgt	tta	att	gcc	gcg	gat	gag	gac	acc	tat	1610
	Leu	Thr	Cys	Asp	Phe	Pro	Arg	Leu	Ile	Ala	Ala	Asp	Glu	Asp	Thr	Tyr	
					480			485					490				
	gag	ccg	atg	gaa	aaa	tac	ttt	ggg	gat	caa	ccg	act	agc	tac	tgg	tgg	1658
	Glu	Pro	Met	Glu	Lys	Tyr	Phe	Gly	Asp	Gln	Pro	Thr	Ser	Tyr	Trp	Trp	
	495				500							505					
	ttt	gtg	aaa	gga	gtg	gaa	gga	tgg	act	ggc	att	gtg	atg	gtt	gtg	cta	1706
	Phe	Val	Lys	Gly	Val	Glu	Gly	Trp	Thr	Gly	Ile	Val	Met	Val	Val	Leu	
	510				515					520					525		
	atg	gct	ata	gcc	ttt	aca	ctc	gct	acg	cct	tgg	ttc	cga	cgt	aac	aag	1754
	Met	Ala	Ile	Ala	Phe	Thr	Leu	Ala	Thr	Pro	Trp	Phe	Arg	Arg	Asn	Lys	
					530					535					540		
	ctt	aac	tta	cct	aac	ttc	ctc	aag	aag	ctt	acc	ggg	ttc	aac	gcc	ttt	1802
	Leu	Asn	Leu	Pro	Asn	Phe	Leu	Lys	Lys	Leu	Thr	Gly	Phe	Asn	Ala	Phe	
					545				550					555			
	tgg	tac	acc	cac	cat	ttg	ttc	atc	att	gtt	tat	gct	ctt	ctc	att	gtc	1850
	Trp	Tyr	Thr	His	His	Leu	Phe	Ile	Ile	Val	Tyr	Ala	Leu	Leu	Ile	Val	
					560			565					570				
	cat	ggg	atc	aag	ctc	tac	ctc	aca	aag	att	tgg	tat	cag	aag	acg	aca	1898
	His	Gly	Ile	Lys	Leu	Tyr	Leu	Thr	Lys	Ile	Trp	Tyr	Gln	Lys	Thr	Thr	
	575				580							585					

tgg	atg	tat	ctt	gct	gta	ccc	atc	ctt	cta	tat	gca	tct	gag	agg	ctg	1946
Trp	Met	Tyr	Leu	Ala	Val	Pro	Ile	Leu	Leu	Tyr	Ala	Ser	Glu	Arg	Leu	
590				595						600					605	
ctc	cgt	gct	ttc	aga	tca	agc	atc	aaa	ccg	gtt	aag	atg	atc	aag	gtg	1994
Leu	Arg	Ala	Phe	Arg	Ser	Ser	Ile	Lys	Pro	Val	Lys	Met	Ile	Lys	Val	
				610					615					620		
gct	gtt	tac	ccc	ggg	aac	gtg	ttg	tct	cta	cac	atg	acg	aag	cca	caa	2042
Ala	Val	Tyr	Pro	Gly	Asn	Val	Leu	Ser	Leu	His	Met	Thr	Lys	Pro	Gln	
			625					630					635			
gga	ttc	aaa	tac	aaa	agt	gga	cag	ttc	atg	ttg	gtg	aac	tgc	cga	gcc	2090
Gly	Phe	Lys	Tyr	Lys	Ser	Gly	Gln	Phe	Met	Leu	Val	Asn	Cys	Arg	Ala	
		640					645					650				
gta	tct	cca	ttc	gaa	tgg	cat	cct	ttc	tca	atc	aca	tca	gct	ccc	gga	2138
Val	Ser	Pro	Phe	Glu	Trp	His	Pro	Phe	Ser	Ile	Thr	Ser	Ala	Pro	Gly	
	655					660					665					
gac	gat	tac	ctg	agc	gta	cat	atc	cgc	act	ctc	ggt	gac	tgg	aca	cgt	2186
Asp	Asp	Tyr	Leu	Ser	Val	His	Ile	Arg	Thr	Leu	Gly	Asp	Trp	Thr	Arg	
	670				675					680					685	
aag	ctc	agg	acc	gtt	ttc	tcc	gag	gtt	tgc	aaa	cct	cct	acc	gcc	ggt	2234
Lys	Leu	Arg	Thr	Val	Phe	Ser	Glu	Val	Cys	Lys	Pro	Pro	Thr	Ala	Gly	
			690						695					700		
aaa	agc	ggt	ctt	ctc	cga	gca	gac	gga	gga	gat	gga	aac	ctc	ccg	ttc	2282
Lys	Ser	Gly	Leu	Leu	Arg	Ala	Asp	Gly	Gly	Asp	Gly	Asn	Leu	Pro	Phe	
			705					710				715				
ccg	aag	gtc	ctt	atc	gac	ggt	cca	tac	ggt	gct	ccc	gca	caa	gac	tac	2330
Pro	Lys	Val	Leu	Ile	Asp	Gly	Pro	Tyr	Gly	Ala	Pro	Ala	Gln	Asp	Tyr	
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Lys	Lys	Tyr	Asp	Val	Val	Leu	Leu	Val	Gly	Leu	Gly	Ile	Gly	Ala	Thr	
	735					740					745					
cct	atg	atc	agt	atc	ctt	aag	gac	atc	atc	aac	aac	atg	aaa	ggt	cct	2426
Pro	Met	Ile	Ser	Ile	Leu	Lys	Asp	Ile	Ile	Asn	Asn	Met	Lys	Gly	Pro	
	750				755					760					765	
gac	cgc	gac	agc	gac	att	gag	aac	aat	aac	agt	aac	aac	aat	agt	aaa	2474
Asp	Arg	Asp	Ser	Asp	Ile	Glu	Asn	Asn	Asn	Ser	Asn	Asn	Asn	Ser	Lys	
			770					775						780		
ggg	ttt	aag	aca	agg	aaa	gct	tat	ttc	tac	tgg	gtg	act	agg	gaa	caa	2522
Gly	Phe	Lys	Thr	Arg	Lys	Ala	Tyr	Phe	Tyr	Trp	Val	Thr	Arg	Glu	Gln	
		785					790					795				
gga	tca	ttc	gag	tgg	ttc	aag	gga	ata	atg	gac	gag	att	tcg	gag	tta	2570
Gly	Ser	Phe	Glu	Trp	Phe	Lys	Gly	Ile	Met	Asp	Glu	Ile	Ser	Glu	Leu	
		800					805					810				
gac	gag	gaa	gga	atc	atc	gag	ctt	cac	aat	tat	tgc	acg	agt	gtg	tac	2618
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Ser	His	Phe	Ala	Lys	Pro	Asn	Trp	Arg	Gln	Val	Tyr	Lys	Lys	Ile	Ala	
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ata	gat	gga	cca	tat	gga	gca	cca	gca	caa	gac	tac	aag	aaa	tat	gag	2511
Ile	Asp	Gly	Pro	Tyr	Gly	Ala	Pro	Ala	Gln	Asp	Tyr	Lys	Lys	Tyr	Glu	
		720					725					730				
gtg	gtt	ttg	ttg	gta	ggc	ctt	gga	att	gga	gct	aca	cca	atg	atc	agt	2559
Val	Val	Leu	Leu	Val	Gly	Leu	Gly	Ile	Gly	Ala	Thr	Pro	Met	Ile	Ser	
		735				740					745					
att	gtt	aaa	gac	att	gtc	aac	aac	atg	aag	gca	atg	gac	gaa	gaa	gaa	2607
Ile	Val	Lys	Asp	Ile	Val	Asn	Asn	Met	Lys	Ala	Met	Asp	Glu	Glu	Glu	
750					755					760					765	
aat	tcc	ttg	gaa	gat	gga	cac	aat	aat	aat	atg	gca	cca	aat	tct	agc	2655
Asn	Ser	Leu	Glu	Asp	Gly	His	Asn	Asn	Asn	Met	Ala	Pro	Asn	Ser	Ser	
				770						775				780		
ccc	aat	att	gca	aaa	aat	aag	ggc	aat	aaa	tca	ggc	tca	gca	agt	gga	2703
Pro	Asn	Ile	Ala	Lys	Asn	Lys	Gly	Asn	Lys	Ser	Gly	Ser	Ala	Ser	Gly	
			785					790					795			
gga	aat	aat	ttc	aat	aca	agg	aga	gca	tat	ttc	tat	tgg	gtt	act	aga	2751
Gly	Asn	Asn	Phe	Asn	Thr	Arg	Arg	Ala	Tyr	Phe	Tyr	Trp	Val	Thr	Arg	
		800					805					810				
gaa	caa	ggc	tca	ttt	gat	tgg	ttc	aaa	ggc	ata	atg	aat	gaa	gct	gct	2799
Glu	Gln	Gly	Ser	Phe	Asp	Trp	Phe	Lys	Gly	Ile	Met	Asn	Glu	Ala	Ala	

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      815                      820                      825
gaa atg gac cat aag gga gta att gaa atg cat aat tat tgt act agt 2847
Glu Met Asp His Lys Gly Val Ile Glu Met His Asn Tyr Cys Thr Ser
830
ggt tat gaa gaa ggt gat gct cgt tct gct ctt att act atg ctt cag 2895
Val Tyr Glu Glu Gly Asp Ala Arg Ser Ala Leu Ile Thr Met Leu Gln
850                      855                      860
tct ctt cac cat gcc aaa aat ggt gtt gac att gtc tct ggc acc aga 2943
Ser Leu His His Ala Lys Asn Gly Val Asp Ile Val Ser Gly Thr Arg
865                      870                      875
ggt aag tca cat ttt gct aaa cct aat tgg cgt aat gtc tac aaa cgc 2991
Val Lys Ser His Phe Ala Lys Pro Asn Trp Arg Asn Val Tyr Lys Arg
880                      885                      890
att gct ctc aac cac cct gag gct aaa gtt ggg gtc ttc tat tgt ggg 3039
Ile Ala Leu Asn His Pro Glu Ala Lys Val Gly Val Phe Tyr Cys Gly
895                      900                      905
gca cca gca ctg acc aaa gaa cta aga caa cac gcc ttg gat ttt tca 3087
Ala Pro Ala Leu Thr Lys Glu Leu Arg Gln His Ala Leu Asp Phe Ser
910                      915                      920                      925
cac aag aca tct acc aag ttt gat ttc cat aaa gaa aat ttt 3129
His Lys Thr Ser Thr Lys Phe Asp Phe His Lys Glu Asn Phe
930                      935
tgagcaaaga atagaccatt aagcagagca ttaaaatttc atcaaaacag ctaaggacac 3189
aggttggtttt atagaagtct accaactctc cctattgtgt acagataatg ttgcacttca 3249
agttgatata tagttgtggt tgtgatgcta gtatattaca aaataataag attattttta 3309
tttgtagtaa aaaaaaaaaa aaaaaaaaaa 3338

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<210> 16

<211> 939

<212> PRT

<213> Nicotiana tabacum

<220>

<221> misc\_feature

<222> (547)..(547)

<223> The 'Xaa' at location 547 stands for Tyr, Cys, Ser, or Phe.

<400> 16

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Asp Thr Glu Ile Ile Gly Asn Asp Arg Ala Ser Tyr Ser Gly Pro Leu
20          25          30
Ser Gly Pro Leu Asn Lys Arg Gly Gly Lys Lys Ser Ala Arg Phe Asn
35          40          45
Ile Pro Glu Ser Thr Asp Ile Gly Thr Ser Val Gly Thr Gly Gly Lys
50          55          60
Ser Asn Asp Asp Ala Tyr Val Glu Ile Thr Leu Asp Val Arg Glu Asp
65          70          75          80
Ser Val Ala Val His Ser Val Lys Thr Ala Gly Gly Asp Asp Val Glu
85          90          95
Asp Pro Glu Leu Ala Leu Leu Ala Lys Gly Leu Glu Lys Lys Ser Thr
100         105         110
Leu Gly Ser Ser Leu Val Arg Asn Ala Ser Ser Arg Ile Arg Gln Val
115         120         125
Ser Gln Glu Leu Arg Arg Leu Ala Ser Leu Asn Lys Arg Pro Ile Pro
130         135         140
Thr Gly Arg Phe Asp Arg Asn Lys Ser Ala Ala Ala His Ala Leu Lys
145         150         155         160
Gly Leu Lys Phe Ile Ser Lys Thr Asp Gly Gly Ala Gly Trp Ala Ala
165         170         175
Val Glu Lys Arg Phe Asp Glu Ile Thr Ala Ser Thr Thr Gly Leu Leu

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Pro	Arg	Ala	Lys	Phe	Gly	Glu	Cys	Ile	Gly	Met	Asn	Lys	Glu	Ser	Lys
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Glu	Phe	Ala	Val	Glu	Leu	Tyr	Asp	Ala	Leu	Ala	Arg	Arg	Arg	Asn	Ile
		210				215					220				
Thr	Thr	Asp	Ser	Ile	Asn	Lys	Ala	Gln	Leu	Lys	Glu	Phe	Trp	Asp	Gln
225					230					235					240
Val	Ala	Asp	Gln	Ser	Phe	Asp	Ser	Arg	Leu	Gln	Thr	Phe	Phe	Asp	Met
				245					250					255	
Val	Asp	Lys	Asp	Ala	Asp	Gly	Arg	Ile	Thr	Glu	Glu	Glu	Val	Arg	Glu
			260					265					270		
Ile	Ile	Gly	Leu	Ser	Ala	Ser	Ala	Asn	Arg	Leu	Ser	Thr	Ile	Gln	Lys
		275					280					285			
Gln	Ala	Asp	Glu	Tyr	Ala	Ala	Met	Ile	Met	Glu	Glu	Leu	Asp	Pro	Asn
		290				295					300				
Asn	Leu	Gly	Tyr	Ile	Met	Ile	Glu	Asn	Leu	Glu	Met	Leu	Leu	Leu	Gln
305					310					315					320
Ala	Pro	Asn	Gln	Ser	Val	Gln	Arg	Gly	Gly	Glu	Ser	Arg	Asn	Leu	Ser
				325					330					335	
Gln	Met	Leu	Ser	Gln	Lys	Leu	Lys	His	Thr	Gln	Glu	Arg	Asn	Pro	Ile
			340					345					350		
Val	Arg	Trp	Tyr	Lys	Ser	Phe	Met	Tyr	Phe	Leu	Leu	Asp	Asn	Trp	Gln
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Arg	Val	Trp	Val	Leu	Leu	Leu	Trp	Ile	Gly	Ile	Met	Ala	Gly	Leu	Phe
		370				375					380				
Thr	Trp	Lys	Tyr	Ile	Gln	Tyr	Lys	Glu	Lys	Ala	Ala	Tyr	Lys	Val	Met
385					390				395						400
Gly	Pro	Cys	Val	Cys	Phe	Ala	Lys	Gly	Ala	Ala	Glu	Thr	Leu	Lys	Leu
				405					410					415	
Asn	Met	Ala	Ile	Ile	Leu	Phe	Pro	Val	Cys	Arg	Asn	Thr	Ile	Thr	Trp
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Leu	Arg	Asn	Lys	Thr	Arg	Leu	Gly	Ala	Ala	Val	Pro	Phe	Asp	Asp	Asn
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Leu	Asn	Phe	His	Lys	Val	Ile	Ala	Val	Ala	Ile	Ala	Leu	Gly	Val	Gly
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Ile	His	Gly	Leu	Ser	His	Leu	Thr	Cys	Asp	Phe	Pro	Arg	Leu	Leu	Asn
465					470					475					480
Ala	Ser	Glu	Glu	Glu	Tyr	Glu	Pro	Met	Lys	Tyr	Tyr	Phe	Gly	Asp	Gln
				485					490					495	
Pro	Glu	Ser	Tyr	Trp	Trp	Phe	Ile	Lys	Gly	Val	Glu	Gly	Val	Thr	Gly
			500					505					510		
Ile	Ile	Met	Val	Val	Leu	Met	Ala	Ile	Ala	Phe	Thr	Leu	Ala	Thr	Pro
		515					520					525			
Trp	Phe	Arg	Arg	Asn	Arg	Val	Ser	Leu	Pro	Lys	Pro	Phe	His	Lys	Leu
		530													

Thr Leu Gly Asp Trp Thr Arg Gln Leu Lys Thr Val Phe Ser Glu Val  
 675 680 685  
 Cys Gln Pro Pro Pro Asn Gly Lys Ser Gly Leu Leu Arg Ala Asp Tyr  
 690 695 700  
 Leu Gln Gly Glu Asn Asn Pro Asn Phe Pro Arg Val Leu Ile Asp Gly  
 705 710 715 720  
 Pro Tyr Gly Ala Pro Ala Gln Asp Tyr Lys Lys Tyr Glu Val Val Leu  
 725 730 735  
 Leu Val Gly Leu Gly Ile Gly Ala Thr Pro Met Ile Ser Ile Val Lys  
 740 745 750  
 Asp Ile Val Asn Asn Met Lys Ala Met Asp Glu Glu Glu Asn Ser Leu  
 755 760 765  
 Glu Asp Gly His Asn Asn Asn Met Ala Pro Asn Ser Ser Pro Asn Ile  
 770 775 780  
 Ala Lys Asn Lys Gly Asn Lys Ser Gly Ser Ala Ser Gly Gly Asn Asn  
 785 790 795 800  
 Phe Asn Thr Arg Arg Ala Tyr Phe Tyr Trp Val Thr Arg Glu Gln Gly  
 805 810 815  
 Ser Phe Asp Trp Phe Lys Gly Ile Met Asn Glu Ala Ala Glu Met Asp  
 820 825 830  
 His Lys Gly Val Ile Glu Met His Asn Tyr Cys Thr Ser Val Tyr Glu  
 835 840 845  
 Glu Gly Asp Ala Arg Ser Ala Leu Ile Thr Met Leu Gln Ser Leu His  
 850 855 860  
 His Ala Lys Asn Gly Val Asp Ile Val Ser Gly Thr Arg Val Lys Ser  
 865 870 875 880  
 His Phe Ala Lys Pro Asn Trp Arg Asn Val Tyr Lys Arg Ile Ala Leu  
 885 890 895  
 Asn His Pro Glu Ala Lys Val Gly Val Phe Tyr Cys Gly Ala Pro Ala  
 900 905 910  
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<220>  
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 <223> coding for NADPH oxidase

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 ggg ttg ccg agg ccg ccg ggg gcg ggg gcg ggt gcg gcg gcg ggc ggg 96  
 Gly Leu Pro Arg Pro Pro Gly Ala Gly Ala Gly Ala Ala Gly Gly  
 20 25 30  
 ttc gcg cgg ggg ctg atg aag cag ccg tcg cgg ctg gcg tcc ggg gtg 144  
 Phe Ala Arg Gly Leu Met Lys Gln Pro Ser Arg Leu Ala Ser Gly Val  
 35 40 45  
 agg cag ttc gcg tcg agg gtg tcg atg aag gtg ccg gag ggg gtg ggg 192  
 Arg Gln Phe Ala Ser Arg Val Ser Met Lys Val Pro Glu Gly Val Gly  
 50 55 60  
 ggg atg cgg ccc ggt ggc ggg agg atg acg cgg atg cag tcc agc gcg 240  
 Gly Met Arg Pro Gly Gly Arg Met Thr Arg Met Gln Ser Ser Ala  
 65 70 75 80

cag	gtg	ggg	ctc	cgg	ggg	ctc	cgc	ttc	ctc	gac	aag	acg	tcc	ggc	ggg	288
Gln	Val	Gly	Leu	Arg	Gly	Leu	Arg	Phe	Leu	Asp	Lys	Thr	Ser	Gly	Gly	
				85					90					95		
aag	gag	ggg	tgg	aag	tcc	gtc	gag	cgc	ctc	gac	gag	atg	aac	cgc		336
Lys	Glu	Gly	Trp	Lys	Ser	Val	Glu	Arg	Arg	Phe	Asp	Glu	Met	Asn	Arg	
			100					105					110			
aac	ggc	cgc	ctc	ccc	aag	gag	agc	ttc	ggc	aag	tgc	atc	ggc	atg	ggg	384
Asn	Gly	Arg	Leu	Pro	Lys	Glu	Ser	Phe	Gly	Lys	Cys	Ile	Gly	Met	Gly	
			115					120				125				
gac	tcc	aag	gag	ttc	gcc	ggc	gag	ctg	ttc	gtg	gcg	ctg	gcg	cgg	cgg	432
Asp	Ser	Lys	Glu	Phe	Ala	Gly	Glu	Leu	Phe	Val	Ala	Leu	Ala	Arg	Arg	
			130			135					140					
agg	aac	ctg	gag	ccg	gag	gac	ggc	atc	acc	aag	gag	cag	ctc	aag	gag	480
Arg	Asn	Leu	Glu	Pro	Glu	Asp	Gly	Ile	Thr	Lys	Glu	Gln	Leu	Lys	Glu	
					150					155					160	
ttc	tgg	gag	gag	atg	acc	gac	cag	aac	ttc	gac	tcg	cgg	ctt	cgc	att	528
Phe	Trp	Glu	Glu	Met	Thr	Asp	Gln	Asn	Phe	Asp	Ser	Arg	Leu	Arg	Ile	
				165					170					175		
ttc	ttt	gac	atg	tgc	gac	aag	aat	ggc	gat	ggg	atg	ctc	acg	gaa	gat	576
Phe	Phe	Asp	Met	Cys	Asp	Lys	Asn	Gly	Asp	Gly	Met	Leu	Thr	Glu	Asp	
			180					185					190			
gag	gtc	aag	gag	gtt	att	ata	ctg	agt	gcg	tcg	gcg	aac	aag	ctg	gcg	624
Glu	Val	Lys	Glu	Val	Ile	Ile	Leu	Ser	Ala	Ser	Ala	Asn	Lys	Leu	Ala	
			195				200					205				
aag	ctg	aag	gga	cac	gcg	gcg	acg	tac	gcg	tcg	ctg	atc	atg	gag	gag	672
Lys	Leu	Lys	Gly	His	Ala	Ala	Thr	Tyr	Ala	Ser	Leu	Ile	Met	Glu	Glu	
			210			215					220					
ctg	gac	ccg	gac	gac	cgc	ggg	tac	atc	gag	atc	tgg	cag	ctg	gag	acg	720
Leu	Asp	Pro	Asp	Asp	Arg	Gly	Tyr	Ile	Glu	Ile	Trp	Gln	Leu	Glu	Thr	
					230				235					240		
ctg	ctg	cgc	ggc	atg	gtg	agc	gcg	cag	gcg	gcg	ccg	gag	aag	atg	aag	768
Leu	Leu	Arg	Gly	Met	Val	Ser	Ala	Gln	Ala	Ala	Pro	Glu	Lys	Met	Lys	
				245					250					255		
cgg	acg	acg	tcg	agc	ctc	gcg	agg	acg	atg	atc	ccg	tcg	cgg	tac	cgg	816
Arg	Thr	Thr	Ser	Ser	Leu	Ala	Arg	Thr	Met	Ile	Pro	Ser	Arg	Tyr	Arg	
			260					265					270			
agc	ccg	ctg	aag	cgg	cac	gtg	tcc	agg	acg	gtg	gac	ttc	gtg	cac	gag	864
Ser	Pro	Leu	Lys	Arg	His	Val	Ser	Arg	Thr	Val	Asp	Phe	Val	His	Glu	
			275				280					285				
aac	tgg	aag	cgg	atc	tgg	ctc	gtc	gcg	ctg	tgg	ctc	gcc	gtc	aac	gtc	912
Asn	Trp	Lys	Arg	Ile	Trp	Leu	Val	Ala	Leu	Trp	Leu	Ala	Val	Asn	Val	
			290			295					300					
ggc	ctc	ttc	gcc	tac	aag	ttc	gag	cag	tac	gag	cgg	cgc	gcc	gcg	ttc	960
Gly	Leu	Phe	Ala	Tyr	Lys	Phe	Glu	Gln	Tyr	Glu	Arg	Arg	Ala	Ala	Phe	
			305		310					315					320	
cag	gtg	atg	ggc	cac	tgc	gtg	tgc	gtg	gcc	aag	ggc	gcc	gcc	gag	gtg	1008
Gln	Val	Met	Gly	His	Cys	Val	Cys	Val	Ala	Lys	Gly	Ala	Ala	Glu	Val	
				325					330					335		
ctc	aag	ctc	aac	atg	gcg	ctc	atc	ctc	ctc	ccc	gtg	tgc	cgg	aac	acg	1056
Leu	Lys	Leu	Asn	Met	Ala	Leu	Ile	Leu	Leu	Pro	Val	Cys	Arg	Asn	Thr	
			340					345					350			
ctc	acc	acg	ctc	agg	tcc	acg	gcg	ctc	agc	cac	gtc	atc	ccc	ttc	gac	1104
Leu	Thr	Thr	Leu	Arg	Ser	Thr	Ala	Leu	Ser	His	Val	Ile	Pro	Phe	Asp	
			355				360					365				
gac	aac	atc	aac	ttc	cac	aag	gtg	atc	gcg	gcg	acc	atc	gcc	gcc	gcc	1152
Asp	Asn	Ile	Asn	Phe	His	Lys	Val	Ile	Ala	Ala	Thr	Ile	Ala	Ala	Ala	
			370			375					380					
acc	gcc	gtc	cac	acg	ctg	gcg	cac	gtc	acc	tgc	gac	ttc	ccg	agg	ctg	1200
Thr	Ala	Val	His	Thr	Leu	Ala	His	Val	Thr	Cys	Asp	Phe	Pro	Arg	Leu	
					390					395					400	
atc	aac	tgc	ccc	agc	gac	aag	ttc	atg	gcg	acg	ctg	ggg	ccg	aac	ttc	1248

Ile	Asn	Cys	Pro	Ser	Asp	Lys	Phe	Met	Ala	Thr	Leu	Gly	Pro	Asn	Phe	
				405					410					415		
ggg	tac	agg	cag	ccg	acg	tac	gcc	gac	ctg	ctg	gag	agc	gcc	ccc	ggc	1296
Gly	Tyr	Arg	Gln	Pro	Thr	Tyr	Ala	Asp	Leu	Leu	Glu	Ser	Ala	Pro	Gly	
				420				425					430			
gtc	acc	ggc	atc	ctc	atg	atc	atc	atc	atg	tcc	ttc	tcc	ttc	acg	ctg	1344
Val	Thr	Gly	Ile	Leu	Met	Ile	Ile	Ile	Met	Ser	Phe	Ser	Phe	Thr	Leu	
		435					440					445				
gcc	acg	cac	tcc	ttc	cgc	cgg	agc	gtc	gtc	aag	ctg	ccg	tcg	ccg	ctg	1392
Ala	Thr	His	Ser	Phe	Arg	Arg	Ser	Val	Val	Lys	Leu	Pro	Ser	Pro	Leu	
	450					455					460					
cac	cac	ctc	gcc	ggc	ttc	aac	gcc	ttc	tgg	tac	gcg	cac	cac	ctc	ctg	1440
His	His	Leu	Ala	Gly	Phe	Asn	Ala	Phe	Trp	Tyr	Ala	His	His	Leu	Leu	
465					470					475					480	
gtg	ctc	gcc	tac	gtc	ctc	ctc	gtc	gtg	cac	tcc	tac	ttc	ata	ttc	ctc	1488
Val	Leu	Ala	Tyr	Val	Leu	Leu	Val	Val	His	Ser	Tyr	Phe	Ile	Phe	Leu	
				485					490					495		
acc	agg	gag	tgg	tac	aag	aaa	acg	aca	tgg	atg	tac	ctg	ata	gtc	cca	1536
Thr	Arg	Glu	Trp	Tyr	Lys	Lys	Thr	Thr	Trp	Met	Tyr	Leu	Ile	Val	Pro	
		500						505					510			
gtg	ctc	ttc	tat	gca	tgc	gag	aga	acg	atc	aga	aaa	gtt	cga	gag	aac	1584
Val	Leu	Phe	Tyr	Ala	Cys	Glu	Arg	Thr	Ile	Arg	Lys	Val	Arg	Glu	Asn	
		515					520					525				
aac	tac	cgc	gtg	agc	atc	gtc	aag	gca	gcg	att	tac	cca	gga	aat	gtg	1632
Asn	Tyr	Arg	Val	Ser	Ile	Val	Lys	Ala	Ala	Ile	Tyr	Pro	Gly	Asn	Val	
	530					535					540					
ctc	tct	ctt	cac	atg	aag	aag	ccg	ccg	ggt	ttc	aag	tac	aag	agc	ggg	1680
Leu	Ser	Leu	His	Met	Lys	Lys	Pro	Pro	Gly	Phe	Lys	Tyr	Lys	Ser	Gly	
545					550					555					560	
atg	tac	ctg	ttt	gtg	aag	tgc	cct	gat	gtc	tct	cct	ttc	gaa	tgg	cat	1728
Met	Tyr	Leu	Phe	Val	Lys	Cys	Pro	Asp	Val	Ser	Pro	Phe	Glu	Trp	His	
				565					570					575		
ccc	ttc	tcc	atc	act	tct	gca	cct	gga	gat	gac	tac	ctg	agt	gtg	cat	1776
Pro	Phe	Ser	Ile	Thr	Ser	Ala	Pro	Gly	Asp	Asp	Tyr	Leu	Ser	Val	His	
				580				585					590			
atc	cgt	aca	cta	ggt	gac	tgg	acg	act	gaa	ctc	aga	aac	ctg	ttt	ggg	1824
Ile	Arg	Thr	Leu	Gly	Asp	Trp	Thr	Thr	Glu	Leu	Arg	Asn	Leu	Phe	Gly	
		595				600						605				
aag	gct	tgc	gag	gca	cag	gtt	act	tct	aag	aag	gct	acc	ctt	tca	aga	1872
Lys	Ala	Cys	Glu	Ala	Gln	Val	Thr	Ser	Lys	Lys	Ala	Thr	Leu	Ser	Arg	
	610					615						620				
ctt	gaa	act	aca	gtt	gtg	gcg	gac	gct	cag	aca	gag	gat	act	agg	ttt	1920
Leu	Glu	Thr	Thr	Val	Val	Ala	Asp	Ala	Gln	Thr	Glu	Asp	Thr	Arg	Phe	
625					630					635					640	
cct	aag	gtc	ctt	att	gat	ggg	ccc	tat	ggt	gca	ccg	gcg	caa	aac	tac	1968
Pro	Lys	Val	Leu	Ile	Asp	Gly	Pro	Tyr	Gly	Ala	Pro	Ala	Gln	Asn	Tyr	
				645					650					655		
aag	aag	tat	gac	att	ctt	ttg	ctt	att	ggt	ctt	gga	att	ggt	gct	act	2016
Lys	Lys	Tyr	Asp	Ile	Leu	Leu	Leu	Ile	Gly	Leu	Gly	Ile	Gly	Ala	Thr	
			660					665					670			
cct	ttc	atc	agc	att	ctg	aag	gat	ctg	ttg	aac	aac	att	aaa	tcc	aac	2064
Pro	Phe	Ile	Ser	Ile	Leu	Lys	Asp	Leu	Leu	Asn	Asn	Ile	Lys	Ser	Asn	
			675				680						685			
gaa	gag	gtg	gaa	agc	ata	cat	ggt	tct	gag	ata	ggc	agc	ttc	aag	aac	2112
Glu	Glu	Val	Glu	Ser	Ile	His	Gly	Ser	Glu	Ile	Gly	Ser	Phe	Lys	Asn	
		690				695					700					
aat	ggg	cca	gga	aga	gct	tac	ttc	tac	tgg	gtg	acc	aga	gag	caa	ggg	2160
Asn	Gly	Pro	Gly	Arg	Ala	Tyr	Phe	Tyr	Trp	Val	Thr	Arg	Glu	Gln	Gly	
705					710					715					720	
tcc	ttc	gag	tgg	ttt	aaa	gga	gtc	atg	aac	gat	gtc	gct	gaa	agt	gat	2208
Ser	Phe	Glu	Trp	Phe	Lys	Gly	Val	Met	Asn	Asp	Val	Ala	Glu	Ser	Asp	



				725					730					735		
cac	aat	aat	att	ata	gag	atg	cac	aat	tac	ctg	acc	agc	gtg	tat	gaa	2256
His	Asn	Asn	Ile	Ile	Glu	Met	His	Asn	Tyr	Leu	Thr	Ser	Val	Tyr	Glu	
			740					745					750			
gaa	ggc	gac	gca	agg	tca	gct	ttg	att	gcc	atg	gtt	cag	tca	ctt	caa	2304
Glu	Gly	Asp	Ala	Arg	Ser	Ala	Leu	Ile	Ala	Met	Val	Gln	Ser	Leu	Gln	
		755					760					765				
cat	gcc	aaa	aat	ggt	gtg	gat	atc	gtc	tcc	ggc	agc	agg	att	cgc	aca	2352
His	Ala	Lys	Asn	Gly	Val	Asp	Ile	Val	Ser	Gly	Ser	Arg	Ile	Arg	Thr	
	770					775					780					
cat	ttt	gcg	agg	cct	aac	tgg	aga	aag	gtg	ttc	tct	gac	ttg	gcg	aat	2400
His	Phe	Ala	Arg	Pro	Asn	Trp	Arg	Lys	Val	Phe	Ser	Asp	Leu	Ala	Asn	
	785				790					795					800	
gcc	cac	aaa	aac	tca	cgc	ata	ggg	gtt	ttc	tat	tgt	gga	tcc	cct	aca	2448
Ala	His	Lys	Asn	Ser	Arg	Ile	Gly	Val	Phe	Tyr	Cys	Gly	Ser	Pro	Thr	
			805						810					815		
ctc	acg	aaa	caa	ctc	aag	gat	ctt	tca	aaa	gaa	ttc	agc	cag	aca	acc	2496
Leu	Thr	Lys	Gln	Leu	Lys	Asp	Leu	Ser	Lys	Glu	Phe	Ser	Gln	Thr	Thr	
			820					825					830			
aca	act	aga	ttc	cac	ttc	cac	aag	gaa	aac	ttt	taa					2532
Thr	Thr	Arg	Phe	His	Phe	His	Lys	Glu	Asn	Phe						
		835					840									

&lt;210&gt; 18

&lt;211&gt; 843

&lt;212&gt; PRT

&lt;213&gt; Oryza sativa

&lt;400&gt; 18

Met	Ala	Ser	Pro	Tyr	Asp	His	Gln	Ser	Pro	His	Ala	Gln	His	Pro	Ser
1				5					10					15	
Gly	Leu	Pro	Arg	Pro	Pro	Gly	Ala	Gly	Ala	Gly	Ala	Ala	Ala	Gly	Gly
			20					25					30		
Phe	Ala	Arg	Gly	Leu	Met	Lys	Gln	Pro	Ser	Arg	Leu	Ala	Ser	Gly	Val
		35					40					45			
Arg	Gln	Phe	Ala	Ser	Arg	Val	Ser	Met	Lys	Val	Pro	Glu	Gly	Val	Gly
	50					55					60				
Gly	Met	Arg	Pro	Gly	Gly	Gly	Arg	Met	Thr	Arg	Met	Gln	Ser	Ser	Ala
	65				70				75						80
Gln	Val	Gly	Leu	Arg	Gly	Leu	Arg	Phe	Leu	Asp	Lys	Thr	Ser	Gly	Gly
			85						90					95	
Lys	Glu	Gly	Trp	Lys	Ser	Val	Glu	Arg	Phe	Asp	Glu	Met	Asn	Arg	
			100					105				110			
Asn	Gly	Arg	Leu	Pro	Lys	Glu	Ser	Phe	Gly	Lys	Cys	Ile	Gly	Met	Gly
		115					120					125			
Asp	Ser	Lys	Glu	Phe	Ala	Gly	Glu	Leu	Phe	Val	Ala	Leu	Ala	Arg	Arg
	130					135					140				
Arg	Asn	Leu	Glu	Pro	Glu	Asp	Gly	Ile	Thr	Lys	Glu	Gln	Leu	Lys	Glu
	145				150					155					160
Phe	Trp	Glu	Glu	Met	Thr	Asp	Gln	Asn	Phe	Asp	Ser	Arg	Leu	Arg	Ile
				165					170					175	
Phe	Phe	Asp	Met	Cys	Asp	Lys	Asn	Gly	Asp	Gly	Met	Leu	Thr	Glu	Asp
			180					185					190		
Glu	Val	Lys	Glu	Val	Ile	Ile	Leu	Ser	Ala	Ser	Ala	Asn	Lys	Leu	Ala
		195					200					205			
Lys	Leu	Lys	Gly	His	Ala	Ala	Thr	Tyr	Ala	Ser	Leu	Ile	Met	Glu	Glu
	210					215					220				
Leu	Asp	Pro	Asp	Asp	Arg	Gly	Tyr	Ile	Glu	Ile	Trp	Gln	Leu	Glu	Thr
	225				230					235					240
Leu	Leu	Arg	Gly	Met	Val	Ser	Ala	Gln	Ala	Pro	Glu	Lys	Met	Lys	
				245					250				255		

Arg	Thr	Thr	Ser	Ser	Leu	Ala	Arg	Thr	Met	Ile	Pro	Ser	Arg	Tyr	Arg		
			260					265					270				
Ser	Pro	Leu	Lys	Arg	His	Val	Ser	Arg	Thr	Val	Asp	Phe	Val	His	Glu		
		275						280					285				
Asn	Trp	Lys	Arg	Ile	Trp	Leu	Val	Ala	Leu	Trp	Leu	Ala	Val	Asn	Val		
	290					295					300						
Gly	Leu	Phe	Ala	Tyr	Lys	Phe	Glu	Gln	Tyr	Glu	Arg	Arg	Ala	Ala	Phe		
305					310					315					320		
Gln	Val	Met	Gly	His	Cys	Val	Cys	Val	Ala	Lys	Gly	Ala	Ala	Glu	Val		
				325					330					335			
Leu	Lys	Leu	Asn	Met	Ala	Leu	Ile	Leu	Leu	Pro	Val	Cys	Arg	Asn	Thr		
			340					345					350				
Leu	Thr	Thr	Leu	Arg	Ser	Thr	Ala	Leu	Ser	His	Val	Ile	Pro	Phe	Asp		
		355						360					365				
Asp	Asn	Ile	Asn	Phe	His	Lys	Val	Ile	Ala	Ala	Thr	Ile	Ala	Ala	Ala		
	370					375					380						
Thr	Ala	Val	His	Thr	Leu	Ala	His	Val	Thr	Cys	Asp	Phe	Pro	Arg	Leu		
385					390					395					400		
Ile	Asn	Cys	Pro	Ser	Asp	Lys	Phe	Met	Ala	Thr	Leu	Gly	Pro	Asn	Phe		
				405					410					415			
Gly	Tyr	Arg	Gln	Pro	Thr	Tyr	Ala	Asp	Leu	Leu	Glu	Ser	Ala	Pro	Gly		
			420					425					430				
Val	Thr	Gly	Ile	Leu	Met	Ile	Ile	Ile	Met	Ser	Phe	Ser	Phe	Thr	Leu		
		435						440					445				
Ala	Thr	His	Ser	Phe	Arg	Arg	Ser	Val	Val	Lys	Leu	Pro	Ser	Pro	Leu		
	450					455					460						
His	His	Leu	Ala	Gly	Phe	Asn	Ala	Phe	Trp	Tyr	Ala	His	His	Leu	Leu		
465					470					475				480			
Val	Leu	Ala	Tyr	Val	Leu	Leu	Val	Val	His	Ser	Tyr	Phe	Ile	Phe	Leu		
				485					490					495			
Thr	Arg	Glu	Trp	Tyr	Lys	Lys	Thr	Thr	Trp	Met	Tyr	Leu	Ile	Val	Pro		
		500						505					510				
Val	Leu	Phe	Tyr	Ala	Cys	Glu	Arg	Thr	Ile	Arg	Lys	Val	Arg	Glu	Asn		
		515						520					525				
Asn	Tyr	Arg	Val	Ser	Ile	Val	Lys	Ala	Ala	Ile	Tyr	Pro	Gly	Asn	Val		
	530					535					540						
Leu	Ser	Leu	His	Met	Lys	Lys	Pro	Pro	Gly	Phe	Lys	Tyr	Lys	Ser	Gly		
545					550					555					560		
Met	Tyr	Leu	Phe	Val	Lys	Cys	Pro	Asp	Val	Ser	Pro	Phe	Glu	Trp	His		
				565					570					575			
Pro	Phe	Ser	Ile	Thr	Ser	Ala	Pro	Gly	Asp	Asp	Tyr	Leu	Ser	Val	His		
			580					585					590				
Ile	Arg	Thr	Leu	Gly	Asp	Trp	Thr	Thr	Glu	Leu	Arg	Asn	Leu	Phe	Gly		
		595						600					605				
Lys	Ala	Cys	Glu	Ala	Gln	Val	Thr	Ser	Lys	Lys	Ala	Thr	Leu	Ser	Arg		
	610					615						620					
Leu	Glu	Thr	Thr	Val	Val	Ala	Asp	Ala	Gln	Thr	Glu	Asp	Thr	Arg	Phe		
625					630					635					640		
Pro	Lys	Val	Leu	Ile	Asp	Gly	Pro	Tyr	Gly	Ala	Pro	Ala	Gln	Asn	Tyr		
				645					650					655			
Lys	Lys	Tyr	Asp	Ile	Leu	Leu	Leu	Ile	Gly	Leu	Gly	Ile	Gly	Ala	Thr		
			660					665					670				
Pro	Phe	Ile	Ser	Ile	Leu	Lys	Asp	Leu	Leu	Asn	Asn	Ile	Lys	Ser	Asn		
		675					680					685					
Glu	Glu	Val	Glu	Ser	Ile	His	Gly	Ser	Glu	Ile	Gly	Ser	Phe	Lys	Asn		
	690					695					700						
Asn	Gly	Pro	Gly	Arg	Ala	Tyr	Phe	Tyr	Trp	Val	Thr	Arg	Glu	Gln	Gly		
705					710					715					720		
Ser	Phe	Glu	Trp	Phe	Lys	Gly	Val	Met	Asn	Asp	Val	Ala	Glu	Ser	Asp		
				725					730					735			
His	Asn	Asn	Ile	Ile	Glu	Met	His	Asn	Tyr	Leu	Thr	Ser	Val	Tyr	Glu		

			740					745					750				
Glu	Gly	Asp	Ala	Arg	Ser	Ala	Leu	Ile	Ala	Met	Val	Gln	Ser	Leu	Gln		
		755					760					765					
His	Ala	Lys	Asn	Gly	Val	Asp	Ile	Val	Ser	Gly	Ser	Arg	Ile	Arg	Thr		
		770					775					780					
His	Phe	Ala	Arg	Pro	Asn	Trp	Arg	Lys	Val	Phe	Ser	Asp	Leu	Ala	Asn		
785					790					795					800		
Ala	His	Lys	Asn	Ser	Arg	Ile	Gly	Val	Phe	Tyr	Cys	Gly	Ser	Pro	Thr		
			805						810					815			
Leu	Thr	Lys	Gln	Leu	Lys	Asp	Leu	Ser	Lys	Glu	Phe	Ser	Gln	Thr	Thr		
		820						825					830				
Thr	Thr	Arg	Phe	His	Phe	His	Lys	Glu	Asn	Phe							
		835					840										

&lt;210&gt; 19

&lt;211&gt; 2604

&lt;212&gt; DNA

&lt;213&gt; Arabidopsis thaliana

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (1)..(2601)

&lt;223&gt; coding for NADPH oxidase

&lt;400&gt; 19

atg	tct	aga	gtg	agt	ttt	gaa	gtg	tca	gga	ggc	tat	cac	tct	gat	gca	48
Met	Ser	Arg	Val	Ser	Phe	Glu	Val	Ser	Gly	Gly	Tyr	His	Ser	Asp	Ala	
1				5					10					15		
gaa	gcc	gga	aac	agc	gga	cca	atg	agc	ggg	ggg	caa	tta	cca	ccg	atc	96
Glu	Ala	Gly	Asn	Ser	Gly	Pro	Met	Ser	Gly	Gly	Gln	Leu	Pro	Pro	Ile	
			20					25					30			
tat	aaa	aaa	ccg	ggg	aac	tcc	aga	ttc	act	gct	gag	aac	agt	cag	aga	144
Tyr	Lys	Lys	Pro	Gly	Asn	Ser	Arg	Phe	Thr	Ala	Glu	Asn	Ser	Gln	Arg	
		35				40						45				
aca	cgt	acg	gca	cca	tac	gtg	gac	ctc	acg	gta	gat	gta	caa	gac	gat	192
Thr	Arg	Thr	Ala	Pro	Tyr	Val	Asp	Leu	Thr	Val	Asp	Val	Gln	Asp	Asp	
	50				55					60						
aca	gtc	tct	gta	cat	agc	ttg	aaa	atg	gaa	ggg	gga	tct	agc	gtt	gaa	240
Thr	Val	Ser	Val	His	Ser	Leu	Lys	Met	Glu	Gly	Gly	Ser	Ser	Val	Glu	
	65				70					75					80	
gag	agt	ccg	gag	ctt	act	ttg	ctg	aaa	cga	aac	cgt	ctt	gag	aag	aaa	288
Glu	Ser	Pro	Glu	Leu	Thr	Leu	Leu	Lys	Arg	Asn	Arg	Leu	Glu	Lys	Lys	
			85						90					95		
aca	acg	gtg	gtg	aaa	cgt	ttg	gcg	tct	gtt	tct	cac	gag	ctt	aag	cgt	336
Thr	Thr	Val	Val	Lys	Arg	Leu	Ala	Ser	Val	Ser	His	Glu	Leu	Lys	Arg	
		100						105					110			
ttg	aca	tct	gtt	tct	ggg	ggg	att	ggg	gga	aga	aag	ccg	cct	cga	ccg	384
Leu	Thr	Ser	Val	Ser	Gly	Gly	Ile	Gly	Gly	Arg	Lys	Pro	Pro	Arg	Pro	
		115				120						125				
gct	aag	tta	gac	cgg	act	aaa	tcc	gcc	gcg	agt	caa	gcg	ttg	aag	gga	432
Ala	Lys	Leu	Asp	Arg	Thr	Lys	Ser	Ala	Ala	Ser	Gln	Ala	Leu	Lys	Gly	
	130					135					140					
ctt	aag	ttc	att	agt	aaa	acc	gac	ggg	ggc	gcc	ggg	tgg	tct	gcc	gtg	480
Leu	Lys	Phe	Ile	Ser	Lys	Thr	Asp	Gly	Gly	Ala	Gly	Trp	Ser	Ala	Val	
	145				150					155					160	
gag	aag	cgg	ttt	aat	cag	att	acc	gcg	act	acc	ggg	gga	cta	ctt	ctt	528
Glu	Lys	Arg	Phe	Asn	Gln	Ile	Thr	Ala	Thr	Thr	Gly	Gly	Leu	Leu	Leu	
			165						170					175		
cgg	aca	aag	ttc	ggg	gaa	tgc	ata	gga	atg	act	tca	aag	gat	ttt	gct	576
Arg	Thr	Lys	Phe	Gly	Glu	Cys	Ile	Gly	Met	Thr	Ser	Lys	Asp	Phe	Ala	
			180					185					190			

ttg gaa ctg ttt gat gca ttg gct aga aga agg aat ata aca ggg gaa	624
Leu Glu Leu Phe Asp Ala Leu Ala Arg Arg Arg Asn Ile Thr Gly Glu	
195 200 205	
gtg att gat gga gat caa cta aag gag ttt tgg gaa caa att aat gat	672
Val Ile Asp Gly Asp Gln Leu Lys Glu Phe Trp Glu Gln Ile Asn Asp	
210 215 220	
caa agt ttt gat tct cgg ctt aag aca ttc ttt gac atg gtg gat aaa	720
Gln Ser Phe Asp Ser Arg Leu Lys Thr Phe Phe Asp Met Val Asp Lys	
225 230 235 240	
gat gct gat ggt aga ctt aca gaa gac gaa gtt aga gag ttg gag agt	768
Asp Ala Asp Gly Arg Leu Thr Glu Asp Glu Val Arg Glu Leu Glu Ser	
245 250 255	
ctt gag act ctg ctt ttg caa gcg gca aca cag tct gtg ata aca agt	816
Leu Glu Thr Leu Leu Gln Ala Thr Gln Ser Val Ile Thr Ser	
260 265 270	
act ggg gag aga aag aat ctg agt cat atg atg agt cag agg ctt aag	864
Thr Gly Glu Arg Lys Asn Leu Ser His Met Met Ser Gln Arg Leu Lys	
275 280 285	
cct acg ttt aac cgc aac ccg ttg aag cga tgg tac cgt ggt ctt aga	912
Pro Thr Phe Asn Arg Asn Pro Leu Lys Arg Trp Tyr Arg Gly Leu Arg	
290 295 300	
ttc ttc ttg tta gac aac tgg caa aga tgt tgg gtt ata gtg cta tgg	960
Phe Phe Leu Leu Asp Asn Trp Gln Arg Cys Trp Val Ile Val Leu Trp	
305 310 315 320	
ttc ata gtt atg gct ata ctc ttc acc tac aaa tat atc caa tac agg	1008
Phe Ile Val Met Ala Ile Leu Phe Thr Tyr Lys Tyr Ile Gln Tyr Arg	
325 330 335	
cgt agc cct gtg tat cca gtg atg ggt gat tgt gtg tgc atg gct aaa	1056
Arg Ser Pro Val Tyr Pro Val Met Gly Asp Cys Val Cys Met Ala Lys	
340 345 350	
ggt gct gca gaa aca gtg aag ctg aac atg gct ttg att ctc tta cct	1104
Gly Ala Ala Glu Thr Val Lys Leu Asn Met Ala Leu Ile Leu Leu Pro	
355 360 365	
gtt tgt aga aac acc atc aca tgg ctt aga aat aag acc agg ttg ggt	1152
Val Cys Arg Asn Thr Ile Thr Trp Leu Arg Asn Lys Thr Arg Leu Gly	
370 375 380	
cgt gtt gtc cca ttt gat gac aat ctc aac ttc cac aag gtt ata gcg	1200
Arg Val Val Pro Phe Asp Asp Asn Leu Asn Phe His Lys Val Ile Ala	
385 390 395 400	
gtg ggg att ata gtt gga gta acg atg cac gcc ggg gca cat tta gcg	1248
Val Gly Ile Ile Val Gly Val Thr Met His Ala Gly Ala His Leu Ala	
405 410 415	
tgt gat ttc ccg cgg tta cta cat gca act cca gag gca tat agg cct	1296
Cys Asp Phe Pro Arg Leu Leu His Ala Thr Pro Glu Ala Tyr Arg Pro	
420 425 430 435	
tta aga cag ttt ttt ggg gat gag caa cca aag agc tac tgg cat ttt	1344
Leu Arg Gln Phe Phe Gly Asp Glu Gln Pro Lys Ser Tyr Trp His Phe	
440 445	
gta aac tcg gta gaa ggt ata acc gga ctt gtg atg gtt ttg tta atg	1392
Val Asn Ser Val Glu Gly Ile Thr Gly Leu Val Met Val Leu Leu Met	
450 455 460	
gcg att gca ttc aca cta gcc acg cct tgg ttc aga aga ggg aag cta	1440
Ala Ile Ala Phe Thr Leu Ala Thr Pro Trp Phe Arg Arg Gly Lys Leu	
465 470 475 480	
aac tat ctt cca gga cca tta aag aaa cta gct agc ttc aat gcc ttc	1488
Asn Tyr Leu Pro Gly Pro Leu Lys Lys Leu Ala Ser Phe Asn Ala Phe	
485 490 495	
tgg tac act cat cat ttg ttt gtc ata gtc tac att ctt ctt gtt gct	1536
Trp Tyr Thr His His Leu Phe Val Ile Val Tyr Ile Leu Val Ala	
500 505 510	
cat gga tac tac ttg tat ctc acc aga gac tgg cac aat aaa acg act	1584

His	Gly	Tyr	Tyr	Leu	Tyr	Leu	Thr	Arg	Asp	Trp	His	Asn	Lys	Thr	Thr	
		515					520					525				
tgg	atg	tat	ttg	gtg	gta	cca	gtg	gtt	cta	tac	gcg	tgt	gaa	agg	ttg	1632
Trp	Met	Tyr	Leu	Val	Val	Pro	Val	Val	Leu	Tyr		Ala	Cys	Glu	Arg	Leu
		530					535					540				
ata	aga	gca	ttc	agg	tcg	agc	atc	aag	gcg	gtg	act	att	agg	aaa	gta	1680
Ile	Arg	Ala	Phe	Arg	Ser	Ser	Ile	Lys	Ala	Val	Thr	Ile	Arg	Lys	Val	
		545				550					555				560	
gca	gtt	tat	cca	gga	aac	gtg	ctg	gca	att	cac	ttg	tca	agg	cct	caa	1728
Ala	Val	Tyr	Pro	Gly	Asn	Val	Leu	Ala	Ile	His	Leu	Ser	Arg	Pro	Gln	
					565					570					575	
aac	ttc	aaa	tac	aag	agt	ggc	caa	tac	atg	ttt	gtt	aac	tgt	gct	gct	1776
Asn	Phe	Lys	Tyr	Lys	Ser	Gly	Gln	Tyr	Met	Phe	Val	Asn	Cys	Ala	Ala	
			580						585					590		
gtt	tct	cca	ttt	gaa	tgg	cat	cca	ttt	tca	atc	aca	tct	gca	cca	caa	1824
Val	Ser	Pro	Phe	Glu	Trp	His	Pro	Phe	Ser	Ile	Thr	Ser	Ala	Pro	Gln	
		595					600						605			
gat	gat	tac	cta	agt	gtt	cac	att	aga	gtt	ctt	ggg	gat	tgg	aca	cga	1872
Asp	Asp	Tyr	Leu	Ser	Val	His	Ile	Arg	Val	Leu	Gly	Asp	Trp	Thr	Arg	
		610				615						620				
gct	ctc	aaa	gga	gtc	ttc	tct	gag	gtg	tgt	aag	cca	cca	ccg	gca	gga	1920
Ala	Leu	Lys	Gly	Val	Phe	Ser	Glu	Val	Cys	Lys	Pro	Pro	Pro	Ala	Gly	
		625				630					635				640	
gtt	agt	ggc	ctg	ctt	aga	gcc	gac	atg	ttg	cat	ggc	gca	aac	aac	ccc	1968
Val	Ser	Gly	Leu	Leu	Arg	Ala	Asp	Met	Leu	His	Gly	Ala	Asn	Asn	Pro	
					645						650				655	
gac	ttc	ccg	aaa	gtc	ttg	att	gat	ggc	cca	tat	ggc	gca	cca	gca	caa	2016
Asp	Phe	Pro	Lys	Val	Leu	Ile	Asp	Gly	Pro	Tyr	Gly	Ala	Pro	Ala	Gln	
			660						665					670		
gac	tac	aag	aag	tac	gag	gtg	gtt	cta	cta	gtt	ggc	ctc	ggg	att	gga	2064
Asp	Tyr	Lys	Lys	Tyr	Glu	Val	Val	Leu	Leu	Val	Gly	Leu	Gly	Ile	Gly	
		675					680					685				
gcc	aca	cca	atg	atc	agt	atc	gtc	aaa	gac	att	gtt	aac	aac	atc	aag	2112
Ala	Thr	Pro	Met	Ile	Ser	Ile	Val	Lys	Asp	Ile	Val	Asn	Asn	Ile	Lys	
		690					695					700				
gcc	aag	gaa	caa	gcc	caa	cta	aac	cga	atg	gag	aac	gga	aca	agc	gaa	2160
Ala	Lys	Glu	Gln	Ala	Gln	Leu	Asn	Arg	Met	Glu	Asn	Gly	Thr	Ser	Glu	
		705				710					715				720	
cca	caa	cga	agt	aag	aaa	gag	agt	ttc	agg	acc	cgt	aga	gct	tac	ttc	2208
Pro	Gln	Arg	Ser	Lys	Lys	Glu	Ser	Phe	Arg	Thr	Arg	Arg	Ala	Tyr	Phe	
					725					730				735		
tat	tgg	gtt	acg	cgt	gag	caa	ggc	tct	ttc	gat	tgg	ttc	aag	aac	ata	2256
Tyr	Trp	Val	Thr	Arg	Glu	Gln	Gly	Ser	Phe	Asp	Trp	Phe	Lys	Asn	Ile	
			740						745					750		
atg	aac	gaa	gtc	gcg	gaa	cga	gat	gcc	aac	cgc	gtc	atc	gaa	atg	cat	2304
Met	Asn	Glu	Val	Ala	Glu	Arg	Asp	Ala	Asn	Arg	Val	Ile	Glu	Met	His	
			755						760					765		
aac	tat	tgt	aca	agt	gtc	tat	gaa	gaa	ggc	gac	gct	cgt	tcc	gca	ctt	2352
Asn	Tyr	Cys	Thr	Ser	Val	Tyr	Glu	Glu	Gly	Asp	Ala	Arg	Ser	Ala	Leu	
		770				775					780					
ata	cat	atg	ctt	caa	tca	cta	aac	cat	gca	aag	aac	ggc	gtc	gac	att	2400
Ile	His	Met	Leu	Gln	Ser	Leu	Asn	His	Ala	Lys	Asn	Gly	Val	Asp	Ile	
						790					795				800	
gtc	tct	gga	aca	aga	gtt	atg	tcc	cat	ttc	gct	aaa	cct	aac	tgg	aga	2448
Val	Ser	Gly	Thr	Arg	Val	Met	Ser	His	Phe	Ala	Lys	Pro	Asn	Trp	Arg	
					805					810					815	
aac	gtt	tac	aag	cgt	ata	gct	atg	gat	cat	cct	aac	acc	aaa	gtt	gga	2496
Asn	Val	Tyr	Lys	Arg	Ile	Ala	Met	Asp	His	Pro	Asn	Thr	Lys	Val	Gly	
			820						825					830		
gtg	ttt	tac	tgt	gga	gca	cca	gca	ttg	aca	aag	gag	cta	agg	cat	cta	2544
Val	Phe	Tyr	Cys	Gly	Ala	Pro	Ala	Leu	Thr	Lys	Glu	Leu	Arg	His	Leu	

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Ala	Leu	Asp	Phe	Thr	His	Lys	Thr Ser Thr Arg Phe Ser Phe His Lys
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Cys Asp Phe Pro Arg Leu	Leu His Ala Thr Pro	Glu Ala Tyr Arg Pro
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His Gly Tyr Tyr Leu Tyr	Leu Thr Arg Asp Trp	His Asn Lys Thr Thr
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Trp Met Tyr Leu Val Val	Pro Val Val Leu Tyr	Ala Cys Glu Arg Leu
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Ile Arg Ala Phe Arg Ser	Ile Lys Ala Val Thr	Ile Arg Lys Val
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Asn Phe Lys Tyr Lys Ser	Gly Gln Tyr Met Phe	Val Asn Cys Ala Ala
	580	585
Val Ser Pro Phe Glu Trp	His Pro Phe Ser Ile	Thr Ser Ala Pro Gln
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Asp Asp Tyr Leu Ser Val	His Ile Arg Val Leu	Gly Asp Trp Thr Arg
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Ala Lys Glu Gln Ala Gln	Leu Asn Arg Met Glu	Asn Gly Thr Ser Glu
	705	710
Pro Gln Arg Ser Lys Lys	Glu Ser Phe Arg Thr	Arg Arg Ala Tyr Phe
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Tyr Trp Val Thr Arg Glu	Gln Gly Ser Phe Asp	Trp Phe Lys Asn Ile
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	770	775
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Ala Thr Thr Ser Asn Tyr Tyr Gly Glu Asp Glu Pro Tyr Val Glu Ile
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Thr Leu Asp Ile His Asp Asp Ser Val Ser Val Tyr Gly Leu Lys Ser
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ccg aac cat cga ggg gcc ggg tct aat tat gag gat caa tcg ctt ctc 240
Pro Asn His Arg Gly Ala Gly Ser Asn Tyr Glu Asp Gln Ser Leu Leu
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Arg Gln Gly Arg Ser Gly Arg Ser Asn Ser Val Leu Lys Arg Leu Ala
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Ser Ser Val Ser Thr Gly Ile Thr Arg Val Ala Ser Ser Val Ser Ser
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Ser Ser Ala Arg Lys Pro Pro Arg Pro Gln Leu Ala Lys Leu Arg Arg
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Lys Thr Asp Gly Val Thr Gly Trp Pro Glu Val Glu Lys Arg Phe Tyr
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Cys	Arg	Asn	Thr	Ile	Thr	Trp	Leu	Arg	Thr	Lys	Thr	Lys	Leu	Ser	Ala		
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Gly	Ile	Ser	Val	Gly	Val	Gly	Ile	His	Ala	Thr	Ser	His	Leu	Ala	Cys		
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Asp	Phe	Pro	Arg	Leu	Ile	Ala	Ala	Asp	Glu	Asp	Gln	Tyr	Glu	Pro	Met		
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Ser	Val	Glu	Gly	Val	Thr	Gly	Ile	Gly	Met	Val	Val	Leu	Met	Thr	Ile		
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Pro	Gly	Pro	Leu	Lys	Lys	Ile	Thr	Gly	Phe	Asn	Ala	Phe	Trp	Tyr	Ser		
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cac	cac	tta	ttt	ggt	atc	gtc	tac	tcg	ctt	ctt	gtc	ggt	cat	gga	ttc	1632	
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tac	gta	tac	ctc	atc	atc	gag	cca	tgg	tac	aag	aaa	acg	aca	tgg	atg	1680	
Tyr	Val	Tyr	Leu	Ile	Ile	Glu	Pro	Trp	Tyr	Lys	Lys	Thr	Thr	Trp	Met		
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tat	ttg	atg	gta	ccg	gtg	ggt	ctt	tac	ttg	tgt	gaa	agg	ctg	att	cgt	1728	
Tyr	Leu	Met	Val	Pro	Val	Val	Leu	Tyr	Leu	Cys	Glu	Arg	Leu	Ile	Arg		
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Thr	Leu	Asp	Ile	His	Asp	Asp	Ser	Val	Ser	Val	Tyr	Gly	Leu	Lys	Ser
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Arg	Gln	Gly	Arg	Ser	Gly	Arg	Ser	Asn	Ser	Val	Leu	Lys	Arg	Leu	Ala
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Ser	Ser	Val	Ser	Thr	Gly	Ile	Thr	Arg	Val	Ala	Ser	Ser	Val	Ser	Ser
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Val	Met	Thr	Met	Thr	Asn	Asn	Gly	Leu	Leu	His	Arg	Ser	Arg	Phe	Gly
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Gly	Glu	Ser	Lys	Lys	Leu	Ser	Lys	Met	Leu	Ser	Gln	Asn	Leu	Met	Val
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Ala	Ala	Glu	Thr	Leu	Lys	Leu	Asn	Met	Ala	Met	Ile	Leu	Leu	Pro	Val
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Cys	Arg	Asn	Thr	Ile	Thr	Trp	Leu	Arg	Thr	Lys	Thr	Lys	Leu	Ser	Ala
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Pro	Pro	Val	Ser	Pro	Ser	Arg	Lys	Ser	Glu	Thr	Phe	Arg	Thr	Lys	Arg
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<223> Description of the artificial sequence:  
oligonucleotide primer

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20

<210> 24  
<211> 21  
<212> DNA  
<213> Artificial sequence

<220>  
<223> Description of the artificial sequence:  
oligonucleotide primer

<400> 24  
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21